

GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 1999, 10:11:21 ; Search time 6413.31 Seconds

(without alignments)  
3185.777 Million cell updates/sec

Title: US-08-798-691A-3

Perfect score: 5711  
Sequence: 1 AGCTGCGTGAACACTTCTG.....TCCCCACAGCCACTACTGA 5711

Scoring table: IDENTITY\_NUC

Searched: 808301 seqs, 1788773984 residues

Database :

GenEmbl:\*  
1: gb\_dal:\*  
2: gb\_ba2:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl1:\*  
9: gb\_pl2:\*  
10: gb\_pr1:\*  
11: gb\_pr2:\*  
12: gb\_pr3:\*  
13: gb\_ro:\*  
14: gb\_st:\*  
15: gb\_sy:\*  
16: gb\_un:\*  
17: gb\_vl:\*  
18: gb\_hcg:\*  
19: em\_ba:\*  
20: em\_fun:\*  
21: em\_hum1:\*  
22: em\_hum2:\*  
23: em\_in:\*  
24: em\_om:\*  
25: em\_or:\*  
26: em\_ov:\*  
27: em\_pat:\*  
28: em\_ph:\*  
29: em\_pl:\*  
30: em\_ro:\*  
31: em\_sy:\*  
32: em\_un:\*  
33: em\_vl:\*  
34: em\_htg:\*  
35: em\_sts:\*  
36: gb\_dal:\*  
37: gb\_ba2:\*  
38: gb\_pl1:\*  
39: gb\_pl2:\*  
40: gb\_pr1:\*  
41: gb\_pr2:\*  
42: gb\_pr3:\*  
43: gb\_sts:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No. Query Match Score Length DB ID Description

1	5711	100.0	5711	6	AR007334
2	5709.4	100.0	5914	6	AR004673
3	5709.4	100.0	5914	6	AR008159
4	5709.4	100.0	5914	6	I76943
5	5709.4	100.0	5914	6	I80938
6	5709.4	100.0	5914	6	I81034
7	5709.4	100.0	5711	10	HSU14680
8	5709.4	100.0	5711	40	HSU14680
9	5707.8	99.9	5711	6	I40795
10	5707.8	99.9	5711	6	I40801
11	5703	99.9	5711	6	AR007335
12	5701.4	99.8	5711	6	AR007333
13	5701.4	99.8	5711	6	I59546
14	5698.4	99.8	5712	6	I40803
15	5697.4	99.8	5710	6	I40797
16	5695.4	99.7	5709	6	I40793
17	5695.4	99.7	5709	6	I40798
18	5695.4	99.7	5709	6	I40799
19	5695.4	99.7	5709	6	I40800
20	5691.4	99.7	5707	6	I40802
21	5685.4	99.0	5689	6	I40794
22	5629.2	98.6	5770	6	I40796
23	5590.4	97.9	5656	6	I40792
24	5532.4	96.9	5693	11	AF005068
25	5532.4	96.9	5693	41	AF005068
26	5387.6	69.8	5637	4	CFU50709
27	3427.4	60.0	117143	12	HUMBCAL
28	3427.4	60.0	117143	42	HUMBCAL
29	3412.2	59.7	4249	6	AR004691
30	3412.2	59.7	4249	6	AR008177
31	3412.2	59.7	4249	6	I76961
32	3412.2	59.7	4249	6	I80956
33	3412.2	59.2	4249	6	I81052
34	3382.8	59.2	3426	12	AF019075
35	3382.8	59.2	3426	42	AF019075
36	3378	59.1	3426	12	AF019076
37	3378	59.1	3426	12	AF019076
38	3326.8	58.3	3426	12	AF019077
39	3326.8	58.3	3426	12	AF019077
40	3165	55.4	3423	12	AF019078
41	3165	55.4	3423	12	AF019078
42	2940.2	51.5	3441	12	AF019079
43	2940.2	51.5	3441	42	AF019079
44	2804.4	49.1	5607	13	AF036760
45	2748.2	48.1	5702	13	MMU31625

## ALIGNMENTS

RESULT 1  
LOCUS AR007334 5711 bp DNA  
DEFINITION AR007334 Sequence 3 from patent US 5750400  
ACCESSION AR007334  
KEYWORDS 93966818  
NID  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J.,  
Scheller,D.B. and Zeng,B.  
TITLE Coding sequences of the human BRCA1 gene  
JOURNAL Patent: US 5750400-A 3 12-MAY 1998;  
FEATURES Location/Qualifiers  
source 1..5711  
BASE COUNT 1956 a 1098 c 1274 g 1383 t  
ORIGIN

Query Match 100.0% Score 5711; DB 6; Length 5711;

```
Best Local Similarity 100.0%; Pred. No. 0;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

Oy	1	AATCGCTGAGACTTCCTGGACCCCGACAGAGCTGAGGGTTCTCGAATTAACCTGGCC	60
Db	1	AGCTCCCTGAGACTTCTTGGACCCCGACAGAGCTGAGGGTTCTCGAATTAACCTGGCC	60
Oy	61	CCTGCGCTCAGAGAGGCGCTTCACCCCTGCTCTGSGGTAAAGTTTCATTGGACAGAAAGAA	120
Db	61	CCGCGCCTCAGAGAGGCGCTTCACCCCTGCTCTGSGGTAAAGTTTCATTGGACAGAAAGAA	120
Oy	121	TGGATTATCTGCTCTTCCGCTTGAACAAAGTAAATGCATTAATGCTATGACAGAAA	180
Db	121	TGGATTATCTGCTCTTCCGCTTGAACAAAGTAAATGCATTAATGCTATGACAGAAA	180
Oy	181	TCTTAGAGTGTCCCATCTGCTCTGAGAGTTGATCAAGAGAACGTCTCCACAAAGTGTACC	240
Db	181	TCTTAGAGTGTCCCATCTGCTCTGAGAGTTGATCAAGAGAACGTCTCCACAAAGTGTACC	240
Oy	241	ACATATTTTGCAAATTTTGCATGCTGAAACTTCTCCAAACGAGACAGAAAGGCGCTTCACAGT	300
Db	241	ACATATTTTGCAAATTTTGCATGCTGAAACTTCTCCAAACGAGACAGAAAGGCGCTTCACAGT	300
Oy	301	GTCCTTATGTAGAAATGATATAACCAAAAGAGCCTACAAAGAAAGTACAGAGATTAGTC	360
Db	301	GTCCTTATGTAGAAATGATATAACCAAAAGAGCCTACAAAGAAAGTACAGAGATTAGTC	360
Oy	361	AACCTTGTGAAGAGCTATTGCAAAATCATTTTGTGCTTTCAAGCTTGACACAGGTTTGAGT	420
Db	361	AACCTTGTGAAGAGCTATTGCAAAATCATTTTGTGCTTTCAAGCTTGACACAGGTTTGAGT	420
Oy	421	ATGCAAAACAGCTAATATTTTGCAGAAAAGAAAATAACTCTCCTGAACATGTAAAGATG	480
Db	421	ATGCAAAACAGCTAATATTTTGCAGAAAAGAAAATAACTCTCCTGAACATGTAAAGATG	480
Oy	481	AAGTTTCTATCATCCAAAGATGATGGGCTACAGAAACGCTGCCAAAAGACTTTCACAGAGTG	540
Db	481	AAGTTTCTATCATCCAAAGATGATGGGCTACAGAAACGCTGCCAAAAGACTTTCACAGAGTG	540
Oy	541	AACCCGAAATCCTTCCTTCGAGAAAACGAGTCCAGATGTCACATCTCTTAACCTTGAA	600
Db	541	AACCCGAAATCCTTCCTTCGAGAAAACGAGTCCAGATGTCACATCTCTTAACCTTGAA	600
Oy	601	CTGTGGAAGCTCTGAGAGACAAGACAGCGGATACAACTCAAAAGACGCTGTCTACATTTG	660
Db	601	CTGTGGAAGCTCTGAGAGACAAGACAGCGGATACAACTCAAAAGACGCTGTCTACATTTG	660
Oy	661	AATGGGATCTGATTTCTTCTGGAAGATCCGTTAATAGGCAACTAATGACAGTGGGAG	720
Db	661	AATGGGATCTGATTTCTTCTGGAAGATCCGTTAATAGGCAACTAATGACAGTGGGAG	720
Oy	721	ATCAGAAATTTGTACAAATCACCCTCTAAGGAACCGAGGATGAATTCAGTTTGGATTCTG	780
Db	721	ATCAGAAATTTGTACAAATCACCCTCTAAGGAACCGAGGATGAATTCAGTTTGGATTCTG	780
Oy	781	CAAAAAGGCTGTTGTGAATTTTCTGAGACGCGATGTAAACAAATCTGAAACATCATCAAC	840
Db	781	CAAAAAGGCTGTTGTGAATTTTCTGAGACGCGATGTAAACAAATCTGAAACATCATCAAC	840
Oy	841	CCAGTAAATATGATTTTGAACACACACATGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAAGT	900
Db	841	CCAGTAAATATGATTTTGAACACACACATGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAAGT	900
Oy	901	ATCAGGATGTTCTGTTTCCAACCTTGCAATGTCATGAGCCATGTGGCAAAATACATCATCCA	960
Db	901	ATCAGGATGTTCTGTTTCCAACCTTGCAATGTCATGAGCCATGTGGCAAAATACATCATCCA	960
Oy	961	GCTCATATTACAGCATGAGACAGAGATTATTAACAATAAGACAGATGATGTAGAAA	1020
Db	961	GCTCATATTACAGCATGAGACAGAGATTATTAACAATAAGACAGATGATGTAGAAA	1020
Oy	1021	AGGCTGAATTTCTGTAAATAAAGCAACAGCCTGAGCTTAGCAAGAGGCAACATTAACAGAT	1080
Db	1021	AGGCTGAATTTCTGTAAATAAAGCAACAGCCTGAGCTTAGCAAGAGGCAACATTAACAGAT	1080

Dd	1021	AGCGTAATTCTGTGTAATATTAAGCAACAGCGTCTGGCTTACGAAAGGCCAACATTAACAT	1089
Qy	1081	GGCGCTGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCAGCACAGAAAAAGGTAG	1140
Dd	1081	GGCGCTGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCAGCACAGAAAAAGGTAG	1140
Qy	1141	ATCTGATGCTGATCCCTGTGTGAGGAAATAATGGAATTAAAGCAAACTGCCATCT	1200
Dd	1141	ATCTGAAAGTGAATCCCTGTGTGAGGAAATAATGGAATTAAAGCAAACTGCCATCT	1200
Qy	1201	CAGAGAACTCAGAGATACAGAGATTTCTCGATTAACCTAAATAGCACATTCAGA	1260
Dd	1201	CAGAGAACTCAGAGATACAGAGATTTCTCGATTAACCTAAATAGCACATTCAGA	1260
Qy	1261	AAGTTAATGAGTGGTTTTCCAGAGATGATMACTGTAGGTTCTGATGACTACATGATG	1320
Dd	1261	AAGTTAATGAGTGGTTTTCCAGAGATGATMACTGTAGGTTCTGATGACTACATGATG	1320
Qy	1321	GGGAGCTGGAATCAATATGCCAAAGTAGCTGATATTGAGCGTTCTAAATGAGTAGTG	1380
Dd	1321	GGGAGCTGGAATCAATATGCCAAAGTAGCTGATATTGAGCGTTCTAAATGAGTAGTG	1380
Qy	1381	AATATCTGGTCTTCAGAGAAATAATGACTTCTGGCCAGTATCCTCATGAGCGTTAA	1440
Dd	1381	AATATCTGGTCTTCAGAGAAATAATGACTTCTGGCCAGTATCCTCATGAGCGTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGATTCACCTCCAAATCAGTAAGAGTAAATTGAGACAAATAAT	1500
Dd	1441	TATGTAAAGTGAAGAGATTCACCTCCAAATCAGTANAGATTAATTGAGACAAATAAT	1500
Qy	1501	TTGGGAAACCTATCGAGAGAGGCAAGCCTCCCACTTAAGCATGTAACTGAAATC	1560
Dd	1501	TTGGGAAACCTATCGAGAGAGGCAAGCCTCCCACTTAAGCATGTAACTGAAATC	1560
Qy	1561	TAAATATGAGGCAATTGTGTACTAGAGCCAGATATACAAAGGCTCCCGCAAAATA	1620
Dd	1561	TAAATATGAGGCAATTGTGTACTAGAGCCAGATATACAAAGGCTCCCGCAAAATA	1620
Qy	1621	AATTAAAGCGTAAAGAGAGACCTACATCAGGCGCTTATCTGAGATTTTATCAAGAG	1680
Dd	1621	AATTAAAGCGTAAAGAGAGACCTACATCAGGCGCTTATCTGAGATTTTATCAAGAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAACCTAACCAACGAGC	1740
Dd	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAACCTAACCAACGAGC	1740
Qy	1741	AGAAATGGTCAAGTATATAAATTACTAATAGTGTCTATGAGATTAACCAAAAGGTGTT	1800
Dd	1741	AGAAATGGTCAAGTATATAAATTACTAATAGTGTCTATGAGATTAACCAAAAGGTGTT	1800
Qy	1801	CTATTCAGAATAGAGAAAAATCCTAACCCCAATGAATCACTGCAAAAAGAAATCTGCTTCA	1860
Dd	1801	CTATTCAGAATAGAGAAAAATCCTAACCCCAATGAATCACTGCAAAAAGAAATCTGCTTCA	1860
Qy	1861	AAAGGAAGCTGAACCTATTAGCAGCAGATATAAGCAATATGCAATCTCAATTAATATCC	1920
Dd	1861	AAAGGAAGCTGAACCTATTAGCAGCAGATATAAGCAATATGCAATCTCAATTAATATCC	1920
Qy	1921	ACAATTCAAAAGCACCTTAATAAGATATGGCTGAGAGAGAGTCTTCTACACGAGATATTC	1980
Dd	1921	ACAATTCAAAAGCACCTTAATAAGATATGGCTGAGAGAGAGTCTTCTACACGAGATATTC	1980
Qy	1981	ATGGGCTGGAACCTAGTGTGATAGTAAGAAATCTAAGCCACCTAATGTGTCAATTGGCAA	2040
Dd	1981	ATGGGCTGGAACCTAGTGTGATAGTAAGAAATCTAAGCCACCTAATGTGTCAATTGGCAA	2040
Qy	2041	TTGTAGTGTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGCGAGTCA	2100
Dd	2041	TTGTAGTGTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGCGAGTCA	2100
Qy	2101	GGCACAGCAGAAACCTACAACTCATGTGAAGGTAAAGACCTTGCAACTGGAGCCAGAAGA	2160
Dd	2101	GGCACAGCAGAAACCTACAACTCATGTGAAGGTAAAGACCTTGCAACTGGAGCCAGAAGA	2160

OY	2161	GTACACAGCCAAATGAAACACACAAAGTAAAGACATGACAGGCATCTCTTCCAGAGCTGA	2220
Db	2161	GTACACAGCCAAATGAAACACACAAAGTAAAGACATGACAGGCATCTCTTCCAGAGCTGA	2220
OY	2221	AGTTAACCAATGACACCTGGTCTTTTACTAAAGTGTCAATATCCAGTAACTTAAAGAT	2280
Db	2221	AGTTAACCAATGACACCTGGTCTTTTACTAAAGTGTCAATATCCAGTAACTTAAAGAT	2280
OY	2281	TTGTCAATCCTAGCCTTCCAGAGAAAGAAAAGAGAAAGTAAACAGTTAAAGT	2340
Db	2281	TTGTCAATCCTAGCCTTCCAGAGAAAGAAAAGAGAAAGTAAACAGTTAAAGT	2340
OY	2341	CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAAAGGTTTTGCCAACTG	2400
Db	2341	CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAAAGGTTTTGCCAACTG	2400
OY	2401	AAAGATCTGTAGAGAGTACAGCATTTTCATTTGTACTGTACTATATGGAACACTGAG	2460
Db	2401	AAAGATCTGTAGAGAGTACAGCATTTTCATTTGTACTGTACTATATGGAACACTGAG	2460
OY	2461	AAATATCTCGTACTCTGGAGTTAGCACTCTAGGGAAGCCAAAACAGACCAATTAAT	2520
Db	2461	AAAGATCTCGTACTCTGGAGTTAGCACTCTAGGGAAGCCAAAACAGACCAATTAAT	2520
OY	2521	GTTGAGTACAGTGTGCAGCATTTTGAAAACCCCAAGGAGTAATTCATGTTGTCCAAAG	2580
Db	2521	GTTGAGTACAGTGTGCAGCATTTTGAAAACCCCAAGGAGTAATTCATGTTGTCCAAAG	2580
OY	2581	ATATATAGAAATGACACAGAGGCTTTTAACTATCATTTGGACATGAAGTTAACACAGTC	2640
Db	2581	ATATATAGAAATGACACAGAGGCTTTTAACTATCATTTGGACATGAAGTTAACACAGTC	2640
OY	2641	GGGAACACAGCATGTGAATGGAAGAAAGTACATGATCTCAGTATTTGGAGAAATCAT	2700
Db	2641	GGGAACACAGCATGTGAATGGAAGAAAGTACATGATCTCAGTATTTGGAGAAATCAT	2700
OY	2701	TCGAAGTTTCAAAGCGCGACATTTTGCTGTGTTTCAAATCCAGGAATCCAGAAAGG	2760
Db	2701	TCGAAGTTTCAAAGCGCGACATTTTGCTGTGTTTCAAATCCAGGAATCCAGAAAGG	2760
OY	2761	AATATGCAACATTTCTCGCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Db	2761	AATATGCAACATTTCTCGCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
OY	2821	TTGATGTGAACAAAGAGAAATCAAGGAAAGATAGTCTAATATCAAGCCTGAC	2880
Db	2821	TTGATGTGAACAAAGAGAAATCAAGGAAAGATAGTCTAATATCAAGCCTGAC	2880
OY	2881	AGACAGTTAATATCTACTGCAAGGCTTTCTGTGTGTGTGCAGAAAGATAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCTACTGCAAGGCTTTCTGTGTGTGTGCAGAAAGATAGCCAGTTGATA	2940
OY	2941	ATGCCAATGTAGATATCAAGGAGGCTCTAGAGTTTGTCTATCATCTAGTTCAGAGGCA	3000
Db	2941	ATGCCAATGTAGATATCAAGGAGGCTCTAGAGTTTGTCTATCATCTAGTTCAGAGGCA	3000
OY	3001	ACGAACATGACATCTATTCTCCAAATPAAACATGAGCTTTTACAAAACCCATATGCTATAC	3060
Db	3001	ACGAACATGACATCTATTCTCCAAATPAAACATGAGCTTTTACAAAACCCATATGCTATAC	3060
OY	3061	CACACATTTTCCATCAACATCTAATTTGTAAACATTAAGTAAAGAAATCTGCTAAGG	3120
Db	3061	CACACATTTTCCATCAACATCTAATTTGTAAACATTAAGTAAAGAAATCTGCTAAGG	3120
OY	3121	AAAACTTTGAGGAACATCTCAATGTCACTCGAAGAGAAATGGAANTGAGAAACATTCGAA	3180
Db	3121	AAAACTTTGAGGAACATCTCAATGTCACTCGAAGAGAAATGGAANTGAGAAACATTCGAA	3180
OY	3181	GTAACAGTACACAAATTAAGCCGTAATTAACATTTAGAGAAATTTTTTAAAGAGCCAGCT	3240
Db	3181	GTAACAGTACACAAATTAAGCCGTAATTAACATTTAGAGAAATTTTTTAAAGAGCCAGCT	3240

QY	3241	CAGGAAATATTAATGAGTAGGTCCAGTACTATAAAGTGGGCTCCAGTATATAAGAA	3300
Db	3241	CAGGAAATATTAATGAGTAGGTCCAGTACTATAAAGTGGGCTCCAGTATATAAGAA	3300
QY	3301	TAGGTTCCAGTAGTGAAGAAATTCACAGACAACTAGGTGAAGAACAGAGGCCAAATATGA	3360
Db	3301	TAGGTTCCAGTAGTGAAGAAATTCACAGACAACTAGGTGAAGAACAGAGGCCAAATATGA	3360
QY	3361	ATGCTATCTTAGATTAGGGGTTTTGCAACCTGAGTCTATAAACAAGCTTCTCTGGAA	3420
Db	3361	ATGCTATCTTAGATTAGGGGTTTTGCAACCTGAGTCTATAAACAAGCTTCTCTGGAA	3420
QY	3421	GTAATTGTAAAGCTCTGGAAATATAAAAAAGCAGAAATATGAAGAGTAGTTCAGACTGTTA	3480
Db	3421	GTAATTGTAAAGCTCTGGAAATATAAAAAAGCAGAAATATGAAGAGTAGTTCAGACTGTTA	3480
QY	3481	ATACAGATTTCCTCCATATCTGATTTCCATATACCTATAGAACGGCTATGGGAAGCTATGC	3540
Db	3481	ATACAGATTTCCTCCATATCTGATTTCCATATACCTATAGAACGGCTATGGGAAGCTATGC	3540
QY	3541	ATGCATCTCAGGTTTGTCTTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAG	3600
Db	3541	ATGCATCTCAGGTTTGTCTTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAG	3600
QY	3601	AAGATACTAGTTTTCGTGAATAATGACATTAGGAAGTTCTGCTGTTTTAGCAAAACG	3660
Db	3601	AAGATACTAGTTTTCGTGAATAATGACATTAGGAAGTTCTGCTGTTTTAGCAAAACG	3660
QY	3661	TCCAGAAAGGAGACTTAGAGAGAGTCTTAGCCCTTCCACCATACACTTTGGTCTCAG	3720
Db	3661	TCCAGAAAGGAGACTTAGAGAGAGTCTTAGCCCTTCCACCATACACTTTGGTCTCAG	3720
QY	3721	GTTACCGAAGAGGGGCCAAGAAATATGAGTCCTCAGAAAGAACTTATCTAGTGAAGAT	3780
Db	3721	GTTACCGAAGAGGGGCCAAGAAATATGAGTCCTCAGAAAGAACTTATCTAGTGAAGAT	3780
QY	3781	AAGAGCTCCCTGCTTCCAACTGTTATTGTGAAGTAAACAAATATACCTCTCAGT	3840
Db	3781	AAGAGCTCCCTGCTTCCAACTGTTATTGTGAAGTAAACAAATATACCTCTCAGT	3840
QY	3841	CTACTAGGCATAGACCGGTGCTACCGAGTGTGCTTAAGAACACAGAGAGAAATTAT	3900
Db	3841	CTACTAGGCATAGACCGGTGCTACCGAGTGTGCTTAAGAACACAGAGAGAAATTAT	3900
QY	3901	TATCATTTAAAGATAGCTTAAATGACTGCGATACAGGTAATATTTGGCAAAAGCATCTC	3960
Db	3901	TATCATTTAAAGATAGCTTAAATGACTGCGATACAGGTAATATTTGGCAAAAGCATCTC	3960
QY	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTCTGCTAGTCTGTTTTCTTCACAGTCA	4020
Db	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTCTGCTAGTCTGTTTTCTTCACAGTCA	4020
QY	4021	GTCGATTGGAAGACTTACTCTGCAATATCAAAACCCAGAGATCCTTCTTGATTTGGTCTT	4080
Db	4021	GTCGATTGGAAGACTTACTCTGCAATATCAAAACCCAGAGATCCTTCTTGATTTGGTCTT	4080
QY	4081	CCAAACAAATAGGCATCACTCTGAAGACGAGGAATTGCTGTAGTGAACAAGAAATTTGG	4140
Db	4081	CCAAACAAATAGGCATCACTCTGAAGACGAGGAATTGCTGTAGTGAACAAGAAATTTGG	4140
QY	4141	TTTCAGATGATGAAGAAAGGAAGCGGCTTGGAAAGAAATATATCAAGAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGGAAGCGGCTTGGAAAGAAATATATCAAGAGCA	4200
QY	4201	TGGAATCAAACCTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAGCGTCTCTGAAG	4260
Db	4201	TGGAATCAAACCTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAGCGTCTCTGAAG	4260
QY	4261	ACTGCTAAGGGCTATCTCTCAAGTAGACATTTTAAACACTAGAGAGGGATACCATGC	4320
Db	4261	ACTGCTAAGGGCTATCTCTCAAGTAGACATTTTAAACACTAGAGAGGGATACCATGC	4320
QY	4321	AACATTAACCTGATTAAGCTTCAGACAGAAATGGCTGAATAGAACCTGTGTTAAACAGC	4380

```

Db 4321 AACATAACCGTATTAACCTCCAGACAGAAATGGTGAACCTGATGTAAGC 4380
Oy 4381 ATGGAGCCAGCCCTTACAGCTACCTTCATCATATAAGTACTCTGCTCCCTGAG 4440
Db 4381 ATGGAGCCAGCCCTTACAGCTACCTTCATCATATAAGTACTCTGCTCCCTGAG 4440
Oy 4441 ACCTGCGAAATCCAGAAACAAAGACATGAAAAAGCAGTATTAACTTCACAGAAAGTA 4500
Db 4441 ACCTGCGAAATCCAGAAACAAAGACATGAAAAAGCAGTATTAACTTCACAGAAAGTA 4500
Oy 4501 GTGAATACCCCTATTAAGCAGAAATCCAGAGGCCCTTCTGCTGACAAAGTTGAGGTCTG 4560
Db 4501 GTGAATACCCCTATTAAGCAGAAATCCAGAGGCCCTTCTGCTGACAAAGTTGAGGTCTG 4560
Oy 4561 CAGATAGTTTACAGTAAATAAAGAACAGAGAGTGAAGAGTCACTCCCTCTTAAT 4620
Db 4561 CAGATAGTTTACAGTAAATAAAGAACAGAGAGTGAAGAGTCACTCCCTCTTAAT 4620
Oy 4621 GCCCATCATTAAGATGATAGTGTGATGACAGAGTGTCTGAGAGTCTTGAATAGAA 4680
Db 4621 GCCCATCATTAAGATGATAGTGTGATGACAGAGTGTCTGAGAGTCTTGAATAGAA 4680
Oy 4681 ACTACCATGTCAGAGAGAGGCTCATTAAGTGTGATGATGAGAGAGCAAGCTGAGAG 4740
Db 4681 ACTACCATGTCAGAGAGAGGCTCATTAAGTGTGATGATGAGAGAGCAAGCTGAGAG 4740
Oy 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTCCAAAGCAGATGTAGAGGAA 4800
Db 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTCCAAAGCAGATGTAGAGGAA 4800
Oy 4801 CCCCTTACCTGGAAATCTGGAATCAAGCTCTCTGATGACCCCTGAATCTGATCCTTGTG 4860
Db 4801 CCCCTTACCTGGAAATCTGGAATCAAGCTCTCTCTGATGACCCCTGAATCTGATCCTTGTG 4860
Oy 4861 AAGACAGAGCCCAAGAGATCGCTGTGTGCAACATACATCTTCAACCTGATGATGA 4920
Db 4861 AAGACAGAGCCCAAGAGATCGCTGTGTGCAACATACATCTTCAACCTGATGATGA 4920
Oy 4921 AAGTCCCAATGAAAGTTGCAAGATCTGCGCAGAGTCCAGTGTCTGCTACTG 4980
Db 4921 AAGTCCCAATGAAAGTTGCAAGATCTGCGCAGAGTCCAGTGTCTGCTACTG 4980
Oy 4981 ATACTGCTGGGTATATGCAATGGAAGAGTGTGAGCAGGAGAGCAGAAATTTGACAG 5040
Db 4981 ATACTGCTGGGTATATGCAATGGAAGAGTGTGAGCAGGAGAGCAGAAATTTGACAG 5040
Oy 5041 CTTCACAGAGAAAGGCTCAACAAAAGATGTCATGTGTGTGCTGCGCTGACCCAGAG 5100
Db 5041 CTTCACAGAGAAAGGCTCAACAAAAGATGTCATGTGTGTGCTGCGCTGACCCAGAG 5100
Oy 5101 AATTATGCTGCTGATCAAGTTGCGCAAAAACACACATCACTTAACTTAATTA 5160
Db 5101 AATTATGCTGCTGATCAAGTTGCGCAAAAACACACATCACTTAACTTAATTA 5160
Oy 5161 CTGAAAGAGTACTCATGTGTGTATGAAAACAGATGCTGATGTGTGTGTAAGGAGC 5220
Db 5161 CTGAAAGAGTACTCATGTGTGTATGAAAACAGATGCTGATGTGTGTGTAAGGAGC 5220
Oy 5221 TGAATATTTTCTAGGAATGCGGAGAGAAATGGGTAGTATTTCTGGGTGACC 5280
Db 5221 TGAATATTTTCTAGGAATGCGGAGAGAAATGGGTAGTATTTCTGGGTGACC 5280
Oy 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTGAAGAGATGAG 5340
Db 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTGAAGAGATGAG 5340
Oy 5341 TCATATGGAAGAAACCAAGAGTCCAAAGGAGAGAGAGATCCAGAGAGAAAGATCT 5400
Db 5341 TCATATGGAAGAAACCAAGAGTCCAAAGGAGAGAGAGATCCAGAGAGAAAGATCT 5400
Oy 5401 TCAGGGGCTAGAAATCTGTGATGAGGCTTACCAACATGCCAGATCAATGAG 5460
Db 5401 TCAGGGGCTAGAAATCTGTGATGAGGCTTACCAACATGCCAGATCAATGAG 5460

```

```

Db 5401 TCAGGGGCTAGAAATCTGTGATGAGGCTTACCAACATGCCAGATCAATGAG 5460
Oy 5461 AATGATGATGACAGCTGTGTGAGTCTGTGTGAGAGAGTTCATATTCACCTTG 5520
Db 5461 AATGATGATGACAGCTGTGTGAGTCTGTGTGAGAGAGTTCATATTCACCTTG 5520
Oy 5521 GCACAGGTGTCCACCAATTTGTGTGTGTGACAGCAGATGCTGTGAGAGAGATGCT 5580
Db 5521 GCACAGGTGTCCACCAATTTGTGTGTGTGACAGCAGATGCTGTGAGAGAGATGCT 5580
Oy 5581 TCCATGCAATTTGGCAGATGATGAGGACCTGTGAGGACCCGAGAGTGTGTGACA 5640
Db 5581 TCCATGCAATTTGGCAGATGATGAGGACCTGTGAGGACCCGAGAGTGTGTGACA 5640
Oy 5641 GTTAGCAGCTTACCAAGTCCAGAGAGTGTGACACCTACCTGATACCCAGATCCCA 5700
Db 5641 GTTAGCAGCTTACCAAGTCCAGAGAGTGTGACACCTACCTGATACCCAGATCCCA 5700
Oy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 2
AR004673 AR004673 5914 bp DNA PAT 04-DEC-1998
LOCUS Sequence 1 from patent US 5747282.
DEFINITION AR004673
ACCESSION AR004673
NID 93965552
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5914)
AUTHORS Skolnick, M.H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A.,
Harsman, K.D., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W.
and Futreal, P. Andrew.
170-linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5747282-A 1 05-MAY-1998;
FEATURES Location/Qualifiers
source 1..5914
BASE COUNT 2006 a 1156 c 1316 g 1436 t
ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5914;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 AGCTCGCTGAGACTTCTGTGACCCGACAGGCTGTGGGTTTCTCAGATTAAGTGGCC 60
Db 1 AGCTCGCTGAGACTTCTGTGACCCGACAGGCTGTGGGTTTCTCAGATTAAGTGGCC 60
Oy 61 CTTGCGCTGAGAGGCTTACCTCTGCTGTGGTAAAGTTCATTTGGAACGAAAGAAA 120
Db 61 CTTGCGCTGAGAGGCTTACCTCTGCTGTGGTAAAGTTCATTTGGAACGAAAGAAA 120
Oy 121 TGGATTATCTGCTCTGCGGTTGGAAGAGTACAAAATGCTAATATGCTATGCAAGAAA 180
Db 121 TGGATTATCTGCTCTGCGGTTGGAAGAGTACAAAATGCTAATATGCTATGCAAGAAA 180
Oy 181 TCTTAGAGTGTCCATCTGCTGAGAGTGTGATCAAGAGAACCTGTCTCCAAAGTGTGAC 240
Db 181 TCTTAGAGTGTCCATCTGCTGAGAGTGTGATCAAGAGAACCTGTCTCCAAAGTGTGAC 240
Oy 241 ACAATATTTTGAATTTTGCAGTGAACCTTCTCAACGAGAAAGAGGCTTACAGT 300
Db 241 ACAATATTTTGAATTTTGCAGTGAACCTTCTCAACGAGAAAGAGGCTTACAGT 300
Oy 301 GTCCCTTATGATAGATGATATTAACCAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360
Db 301 GTCCCTTATGATAGATGATATTAACCAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360

```



QY 361 AACTGTTGAGAGCTATTGAAATCATTTGTGCTTTCAGCTTGACACAGGTTTGAGT 420  
| | | | |  
Db 361 AACTGTTGAGAGCTATTGAAATCATTTGTGCTTTCAGCTTGACACAGGTTTGAGT 420  
QY 421 ATGCAACAGCATTAATTTTGGAAAAAGAAAAATACTCTCTGTAACATCTAAAGATG 480  
| | | | |  
Db 421 ATGCAACAGCATTAATTTTGGAAAAAGAAAAATACTCTCTGTAACATCTAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAAGACTTCTACAGATG 540  
| | | | |  
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAAGACTTCTACAGATG 540  
QY 541 AACCAGAAAAATCTCTCTTCGAGGAAACCAAGCTCTAGTGTCCACTCTCTAACTCTGAA 600  
| | | | |  
Db 541 AACCAGAAAAATCTCTCTTCGAGGAAACCAAGCTCTAGTGTCCACTCTCTAACTCTGAA 600  
QY 601 CTGTGAGAACTCTGAGCAAGCAAGCGGATPACACCTCAAAAGAGCTGTCTCATGTG 660  
| | | | |  
Db 601 CTGTGAGAACTCTGAGCAAGCAAGCGGATPACACCTCAAAAGAGCTGTCTCATGTG 660  
QY 661 AATTGGGATCTGATTCCTCTGAGATACCGTTAATAAGCAACTATTTGCAGTGGAG 720  
| | | | |  
Db 661 AATTGGGATCTGATTCCTCTGAGATACCGTTAATAAGCAACTATTTGCAGTGGAG 720  
QY 721 ATCAAGAAATTTTACAAATCACCCCTCAAGGAACCGGATGAAATCAGTTTGATCTG 780  
| | | | |  
Db 721 ATCAAGAAATTTTACAAATCACCCCTCAAGGAACCGGATGAAATCAGTTTGATCTG 780  
QY 781 CAAAAAGGCGCTTGATTAATTTTCTGAGAGGATPACAAATPCTAATCATCTAAC 840  
| | | | |  
Db 781 CAAAAAGGCGCTTGATTAATTTTCTGAGAGGATPACAAATPCTAATCATCTAAC 840  
QY 841 CCAGTAAATATGATTTGGAACCACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
| | | | |  
Db 841 CCAGTAAATATGATTTGGAACCACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
QY 901 ATCAGGGATGTTCTGTTCAAACTTGCAATGTGAGACCATGTGGCCAAATACTATGCCA 960  
| | | | |  
Db 901 ATCAGGGATGTTCTGTTCAAACTTGCAATGTGAGACCATGTGGCCAAATACTATGCCA 960  
QY 961 GCTATTACAGCATGAGAACAGCGATTATATCTACCTAAAGACAGATGATGAGAA 1020  
| | | | |  
Db 961 GCTATTACAGCATGAGAACAGCGATTATATCTACCTAAAGACAGATGATGAGAA 1020  
QY 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGGCTTACAGAGGAGCCAAATACAGAT 1080  
| | | | |  
Db 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGGCTTACAGAGGAGCCAAATACAGAT 1080  
QY 1081 GGGCTGCAAGTAAAGAAACATGTAATGATGAGCGGACTCCAGACAGAAAAAGGTAG 1140  
| | | | |  
Db 1081 GGGCTGCAAGTAAAGAAACATGTAATGATGAGCGGACTCCAGACAGAAAAAGGTAG 1140  
QY 1141 ATCGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAAACTGCCATGCT 1200  
| | | | |  
Db 1141 ATCGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAAACTGCCATGCT 1200  
QY 1201 CAGAGAAATCTAGAGATACTAGATGTTCTTGATTAACACTAAATAGCAGACTTGA 1260  
| | | | |  
Db 1201 CAGAGAAATCTAGAGATACTAGATGTTCTTGATTAACACTAAATAGCAGACTTGA 1260  
QY 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTATGAACTGTAGTTGATGATCTACATGATG 1320  
| | | | |  
Db 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTATGAACTGTAGTTGATGATCTACATGATG 1320  
QY 1321 GGGAGTCTGATCAAAATGSCAAAGTATGATGATTTGAGAGTTCTAAATAGAGTATG 1380  
| | | | |  
Db 1321 GGGAGTCTGATCAAAATGSCAAAGTATGATGATTTGAGAGTTCTAAATAGAGTATG 1380  
QY 1381 AATATTCGTTCTTCAGAGAAATAGACTTACTGCCAGTATCCATGAGGCTTTAA 1440  
| | | | |  
Db 1381 AATATTCGTTCTTCAGAGAAATAGACTTACTGCCAGTATCCATGAGGCTTTAA 1440

QY 1441 TATGTAAATGGAAGAGTTTACTTCCAAATCAGTAGAGATTAATTTGAACAAATAT 1500  
| | | | |  
Db 1441 TATGTAAATGGAAGAGTTTACTTCCAAATCAGTAGAGATTAATTTGAACAAATAT 1500  
QY 1501 TTGGGAAACCTATCGGAAAGAGGAGGCTCCCAACTTAAAGCATTAAGCTAAGTAAATC 1560  
| | | | |  
Db 1501 TTGGGAAACCTATCGGAAAGAGGAGGCTCCCAACTTAAAGCATTAAGCTAAGTAAATC 1560  
QY 1561 TAATTAATGAGCATTTTGTACTGAGCCACAGATAATACAGAGGCTCCCTCACAAATA 1620  
| | | | |  
Db 1561 TAATTAATGAGCATTTTGTACTGAGCCACAGATAATACAGAGGCTCCCTCACAAATA 1620  
QY 1621 AATTAAAGCTTAAAGAGGAGACTTACATCAGGCTTTCATCTGAGATTTTATCAAGAA 1680  
| | | | |  
Db 1621 AATTAAAGCTTAAAGAGGAGACTTACATCAGGCTTTCATCTGAGATTTTATCAAGAA 1680  
QY 1681 CAGATTTGGCAGTTCAAAAGAGCTGTGAAATGATTAATCAGGGAACCTAACAAAGGAGC 1740  
| | | | |  
Db 1681 CAGATTTGGCAGTTCAAAAGAGCTGTGAAATGATTAATCAGGGAACCTAACAAAGGAGC 1740  
QY 1741 AGAATGCTCAAGTATGATTAATTAATTAAGTGTGATGAGATTAACAAAGGAGTAT 1800  
| | | | |  
Db 1741 AGAATGCTCAAGTATGATTAATTAATTAAGTGTGATGAGATTAACAAAGGAGTAT 1800  
QY 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTGAAAAAGAAATCTGTTCA 1860  
| | | | |  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTGAAAAAGAAATCTGTTCA 1860  
QY 1861 AAAGGAAAGCTGAACCTTAATAGCAGCATTAACCAATATGGAATCGAATTAATATCC 1920  
| | | | |  
Db 1861 AAAGGAAAGCTGAACCTTAATAGCAGCATTAACCAATATGGAATCGAATTAATATCC 1920  
QY 1921 ACAATTCAAAAAGCACCTTAAAAAGATAGGCTGAGAGGAAAGTCTTCTACAGGATATTC 1980  
| | | | |  
Db 1921 ACAATTCAAAAAGCACCTTAAAAAGATAGGCTGAGAGGAAAGTCTTCTACAGGATATTC 1980  
QY 1981 ATGCGCTTGAACCTAGTATGCTAGTAAATCTAACCCCACTTAATTTGTAATGTCAAA 2040  
| | | | |  
Db 1981 ATGCGCTTGAACCTAGTATGCTAGTAAATCTAACCCCACTTAATTTGTAATGTCAAA 2040  
QY 2041 TTGATATGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTAAACCAATGGCAGTCA 2100  
| | | | |  
Db 2041 TTGATATGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTAAACCAATGGCAGTCA 2100  
QY 2101 GGCACAGCAGAAACCTTCAACTCATGGAAGTAAAGAACTGCAACTGAGGCCAAGAA 2160  
| | | | |  
Db 2101 GGCACAGCAGAAACCTTCAACTCATGGAAGTAAAGAACTGCAACTGAGGCCAAGAA 2160  
QY 2161 GTAAACAAGCCAAATGAACAGACAAATGAAGACATGACAGGATACCTTCCAGAGCTGA 2220  
| | | | |  
Db 2161 GTAAACAAGCCAAATGAACAGACAAATGAAGACATGACAGGATACCTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAAATGACACCTGCTTCTTTACTAAGTGTCAATATACAGTAAAGAT 2280  
| | | | |  
Db 2221 AGTTAAACAAATGACACCTGCTTCTTTACTAAGTGTCAATATACAGTAAAGAT 2280  
QY 2281 TTGTCAATCTAGCCTTCCAAAGAGAAAGAAAGAACTGAAGAAAGTTAAAGGT 2340  
| | | | |  
Db 2281 TTGTCAATCTAGCCTTCCAAAGAGAAAGAAAGAAAGAACTGAAGAAAGTTAAAGGT 2340  
QY 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAAACTG 2400  
| | | | |  
Db 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAAACTG 2400  
QY 2401 AAAGATCTGTAAGAGATGAGATTTTCAATGTAAGTGTGATGATTTATGAGCTAGG 2460  
| | | | |  
Db 2401 AAAGATCTGTAAGAGATGAGATTTTCAATGTAAGTGTGATGATTTATGAGCTAGG 2460  
QY 2461 AAAGTATCTGTTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAAAGCAACCAATTAAT 2520  
| | | | |  
Db 2461 AAAGTATCTGTTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAAAGCAACCAATTAAT 2520  
QY 2521 GTGTAGTCAAGTGTGACGACTTTGAAAAACCCCAAGGAGCTAATTCATGTTGTTCCAAAG 2580  
| | | | |

|||||  
Db 2521 GTGAGTCATGTGACACATTTGAAAACCCCAAGGACTAATTATGTTGTTCCAAAG 2580  
OY 2581 ATATAGAAATGACACAGAAAGCCTTTAAGTATCCATTGGGACATGAAGTTAAACCAAGTC 2640  
Db 2581 ATATAGAAATGACACAGAAAGCCTTTAAGTATCCATTGGGACATGAAGTTAAACCAAGTC 2640  
OY 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTGATGCTCAGTATTTGGCAATACAT 2700  
Db 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTGATGCTCAGTATTTGGCAATACAT 2700  
OY 2701 TCAAGGTTTCAAGGCGCCAGTCATTTGCTGTTTCAAAATCCAGGAATGAGAGAGAG 2760  
Db 2701 TCAAGGTTTCAAGGCGCCAGTCATTTGCTGTTTCAAAATCCAGGAATGAGAGAGAG 2760  
OY 2761 AATGTGCAACATCTCTCTGCCCCACTCTGGGTCCTTAAGAAACAAAGTCCAAAAGTCATT 2820  
Db 2761 AATGTGCAACATCTCTCTGCCCCACTCTGGGTCCTTAAGAAACAAAGTCCAAAAGTCATT 2820  
OY 2821 TTGCAATGTGAACAAAGGAAGAAATCAAGGAAGATGAGTCTAATATCAAGCCTGTAC 2880  
Db 2821 TTGCAATGTGAACAAAGGAAGAAATCAAGGAAGATGAGTCTAATATCAAGCCTGTAC 2880  
OY 2881 AGACAGTTAATATCATCTGACAGGCTTTCCTGTGTGTGTCAGAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCATCTGACAGGCTTTCCTGTGTGTGTCAGAAAGATAAGCCAGTTGATA 2940  
OY 2941 ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
OY 3001 ACGAACTGTGACTATCTCTCAAAATCAATGACCTTTTACAAAACCCATATGCTATAC 3060  
Db 3001 ACGAACTGTGACTATCTCTCAAAATCAATGACCTTTTACAAAACCCATATGCTATAC 3060  
OY 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAAACCTAATGTAGAAAAATCTGTAGAG 3120  
Db 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAAACCTAATGTAGAAAAATCTGTGTAGAG 3120  
OY 3121 AAAACTTTGAGGAACATTCATGTCACCTGAAAAGAAATGGGAATGAGAACATTCGA 3180  
Db 3121 AAAACTTTGAGGAACATTCATGTCACCTGAAAAGAAATGGGAATGAGAACATTCGA 3180  
OY 3181 GTACAGTACGACAAATTAAGCCGTATATACATTAGAGAAATGTTTAAAGAAAGCCACT 3240  
Db 3181 GTACAGTACGACAAATTAAGCCGTATATACATTAGAGAAATGTTTAAAGAAAGCCACT 3240  
OY 3241 CAAGCAATATTAATGAAGTAGTCCAGTACATTAATGAAGTGGGCTCCAGTATTAATGA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGTCCAGTACATTAATGAAGTGGGCTCCAGTATTAATGA 3300  
OY 3301 TAGGTTCCAGTATGAAGAAACATTCAGAGCAGAACTAGTGAAGAACAGAGGCCAAAATGA 3360  
Db 3301 TAGGTTCCAGTATGAAGAAACATTCAGAGCAGAACTAGTGAAGAACAGAGGCCAAAATGA 3360  
OY 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTATATAAAAGTCTTCTGTGAA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTATATAAAAGTCTTCTGTGAA 3420  
OY 3421 GTAATTTAAGCATCTGAAATTAATAAAAGCAAGAAATGAGAAATAGTATGCACTGTTA 3480  
Db 3421 GTAATTTAAGCATCTGAAATTAATAAAAGCAAGAAATGAGAAATAGTATGCACTGTTA 3480  
OY 3481 ATACAGATTTCTCTCATATCTGATTTCAATTAAGTAAAGCCATAGGAAAGTATGTC 3540  
Db 3481 ATACAGATTTCTCTCATATCTGATTTCAATTAAGTAAAGCCATAGGAAAGTATGTC 3540  
OY 3541 ATGCAATCTCAGGTTTGTCTGAGACACCTGATGACCTGTATGATGATGTTGAAATGAAG 3600  
Db 3541 ATGCAATCTCAGGTTTGTCTGAGACACCTGATGACCTGTATGATGATGTTGAAATGAAG 3600  
OY 3601 AAGATCTAGTTTGTGAAAATGACATTAAGAAAGTTCGCTGTTTAAAGCAAAAGCG 3660  
|||||

Db 3601 AAGATCTAGTTTGTGAAAATGACATTAAGAAAGTTCGCTGTTTAAAGCAAAAGCG 3660  
OY 3661 TCCAGAAAGAGAGCTTAGACAGAGTCCAGCCCTTTCACCCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAAAGAGAGCTTAGACAGAGTCCAGCCCTTTCACCCATACATTTGGCTCAGG 3720  
OY 3721 GTTACCGAAGAGGGGCCAAAGAAATTAAGAGTCCCTCAGAAAGAAATTTATAGTAGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAAGAAATTAAGAGTCCCTCAGAAAGAAATTTATAGTAGATG 3780  
OY 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTGGTAAAGTAAACAAATATCCTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTGGTAAAGTAAACAAATATCCTCTCAGT 3840  
OY 3841 GTACTAGGCATAGCACCCGTTGCTACCGAGTCTGTCTAAGAACACAGAGAGATTTAT 3900  
Db 3841 GTACTAGGCATAGCACCCGTTGCTACCGAGTCTGTCTAAGAACACAGAGAGATTTAT 3900  
OY 3901 TATCATTAAGAAATAGCTTAATATGATGCTGAGTAAACAGGTAAATTTGGCAAGCATCTC 3960  
Db 3901 TATCATTAAGAAATAGCTTAATATGATGCTGAGTAAACAGGTAAATTTGGCAAGCATCTC 3960  
OY 3961 AGAATCATCACCTTAGTGAAGAAACAAATGTCTGCTAGCTTTTCTTCAAGTGA 4020  
Db 3961 AGAATCATCACCTTAGTGAAGAAACAAATGTCTGCTAGCTTTTCTTCAAGTGA 4020  
OY 4021 GTGAATGGAAGACTTGACTGCAAAATCAAAACACCAGAGTCTTTCTTGAATGGTCTT 4080  
Db 4021 GTGAATGGAAGACTTGACTGCAAAATCAAAACACCAGAGTCTTTCTTGAATGGTCTT 4080  
OY 4081 CCAAAACAAATGAGCATAGCTGAAAGCCGAGAGTGGCTGAGTGAAGCAAGAAATGG 4140  
Db 4081 CCAAAACAAATGAGCATAGCTGAAAGCCGAGAGTGGCTGAGTGAAGCAAGAAATGG 4140  
OY 4141 TTTGATGATGAGAAAGAGAAAGAGGAGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200  
Db 4141 TTTGATGATGAGAAAGAGAAAGAGGAGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200  
OY 4201 TGGATTCAACTTAGTGAAGACACATCTGGGTGTGAGAGTGAAGAAAGAGGCTCTGAG 4260  
Db 4201 TGGATTCAACTTAGTGAAGACACATCTGGGTGTGAGAGTGAAGAAAGAGGCTCTGAG 4260  
OY 4261 ACTGCTAGGGGCTATCCCTCCAGAGTGAACATTTTAACCATCAGCAGAGGATACCATGC 4320  
Db 4261 ACTGCTAGGGGCTATCCCTCCAGAGTGAACATTTTAACCATCAGCAGAGGATACCATGC 4320  
OY 4321 AACATTAACCTGATTAAGGCTCCAGCAGAAATGAGCTGAAAGCTGTGAAGACAGC 4380  
Db 4321 AACATTAACCTGATTAAGGCTCCAGCAGAAATGAGCTGAAAGCTGTGAAGACAGC 4380  
OY 4381 ATGGAGCGACGCTTCTAAGCTACGCTACCTTCATCATTAAGTGAAGTCTTGCCTTGAGG 4440  
Db 4381 ATGGAGCGACGCTTCTAAGCTACGCTACCTTCATCATTAAGTGAAGTCTTGCCTTGAGG 4440  
OY 4441 ACCTCGCAAAATCCAGAAACAAAGCAGATCAGAAAAAGCAGATTAATCTTCACAAAAAGTA 4500  
Db 4441 ACCTCGCAAAATCCAGAAACAAAGCAGATCAGAAAAAGCAGATTAATCTTCACAAAAAGTA 4500  
OY 4501 GTGAATACCTTATTAAGCAGAAATCCAGAAAGGCTTTTGTCTGACAAAGTTGAGGTGCTG 4560  
Db 4501 GTGAATACCTTATTAAGCAGAAATCCAGAAAGGCTTTTGTCTGACAAAGTTGAGGTGCTG 4560  
OY 4561 CAGATAGTTCTTACAGTAAATAATTAAGAACAGAGTGAAGAGTCAATCCCTTTTAAT 4620  
Db 4561 CAGATAGTTCTTACAGTAAATAATTAAGAACAGAGTGAAGAGTCAATCCCTTTTAAT 4620  
OY 4621 GCCCATATTAGATGATAGTGGTACATGCAAGATGCTCTGAGAGCTTCACAAATAGAA 4680  
Db 4621 GCCCATATTAGATGATAGTGGTACATGCAAGATGCTCTGAGAGCTTCACAAATAGAA 4680  
OY 4681 ACTAACCATCTCAAGAGAGAGCTCATTAAGGTTGTGATGAGAGACACACAGCTGGAAG 4740  
Db 4681 ACTAACCATCTCAAGAGAGAGCTCATTAAGGTTGTGATGAGAGACACACAGCTGGAAG 4740

```

QY 4741 AGCTGGGCGCACGATTTGACGGAAACATCTTACTTGCACAAAGCGAAGATCTAGAGGAA 4800
    |||||
Db 4741 AGCTGGGCGCACGATTTGACGGAAACATCTTACTTGCACAAAGCGAAGATCTAGAGGAA 4800
QY 4801 CCCCTTACCTGGAAATCGACGCTCTCTCTGATGACCCGTAATCTGATCTCTG 4860
    |||||
Db 4801 CCCCTTACCTGGAAATCGACGCTCTCTCTGATGACCCGTAATCTGATCTCTG 4860
QY 4861 AAGACAGAGCCCCAGAGTCAGCTGTTGGCAACATCATCTTCAACCTTCGATGA 4920
    |||||
Db 4861 AAGACAGAGCCCCAGAGTCAGCTGTTGGCAACATCATCTTCAACCTTCGATGA 4920
QY 4921 AAGTCCCAATTTGAAGCTTGCAGATCTGCCAGAGTCGACCTGCTCTACTACTG 4980
    |||||
Db 4921 AAGTCCCAATTTGAAGCTTGCAGATCTGCCAGAGTCGACCTGCTCTACTACTG 4980
QY 4981 ATACTGCTGGGATTAATGCAATGGAAGAAAGTGAAGAGGAGGAGAAAGCCAGATTCAG 5040
    |||||
Db 4981 ATACTGCTGGGATTAATGCAATGGAAGAAAGTGAAGAGGAGGAGGAGGAGGAGGAG 5040
QY 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGCTGCTGCTGACCCAGAG 5100
    |||||
Db 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGCTGCTGCTGACCCAGAG 5100
QY 5101 AATTATGCTGCTGACAAAGTTGCCAGAAACACACATCATCTTAACTAATTA 5160
    |||||
Db 5101 AATTATGCTGCTGACAAAGTTGCCAGAAACACACATCATCTTAACTAATTA 5160
QY 5161 CTGAAGAGACTACTGATGTTGTTATGAAGAAAGATGTCAGATGTTGTTGTAAGGAGAC 5220
    |||||
Db 5161 CTGAAGAGACTACTGATGTTGTTATGAAGAAAGATGTCAGATGTTGTTGTAAGGAGAC 5220
QY 5221 TGAATATTTTCTAGGAATGCGGAGAGAAATGGGTAGTTAGTATTTCTGGGACCC 5280
    |||||
Db 5221 TGAATATTTTCTAGGAATGCGGAGAGAAATGGGTAGTTAGTATTTCTGGGACCC 5280
QY 5281 AGCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTTGG 5340
    |||||
Db 5281 AGCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTTGG 5340
QY 5341 TCAATGGAAGAACCCAGAGGTCGCAAGCGAGCAAGAAATCCAGAGACAGAAAGATCT 5400
    |||||
Db 5341 TCAATGGAAGAACCCAGAGGTCGCAAGCGAGCAAGAAATCCAGAGACAGAAAGATCT 5400
QY 5401 TCAGGGGCTAGAAATCTGTTGCTATGCGCCCTTCAACCAATGCCCCACAGATCTGG 5460
    |||||
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGCGCCCTTCAACCAATGCCCCACAGATCTGG 5460
QY 5461 AATGAGTGAACAGCTGTGTGTGCTTGTGTGTAAGAGAGCTTTCATTCACCTTGG 5520
    |||||
Db 5461 AATGAGTGAACAGCTGTGTGTGCTTGTGTGTAAGAGAGCTTTCATTCACCTTGG 5520
QY 5521 GCACAGGTGTCACCCATTTGCTGTTGTCAGCCAGATGCTTGGGACAGAGCAATGCTT 5580
    |||||
Db 5521 GCACAGGTGTCACCCATTTGCTGTTGTCAGCCAGATGCTTGGGACAGAGCAATGCTT 5580
QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGTACCCGAGAGTGGGTGTGGACA 5640
    |||||
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGTACCCGAGAGTGGGTGTGGACA 5640
QY 5641 GTGTAAGCACTTACCAAGTCCAGAGAGTGAACACTTACCTGATACCCAGATCCCCACA 5700
    |||||
Db 5641 GTGTAAGCACTTACCAAGTCCAGAGAGTGAACACTTACCTGATACCCAGATCCCCACA 5700
QY 5701 GCCACTACTGA 5711
    |||||
Db 5701 GCCACTACTGA 5711

```

RESULT 3  
AR008159  
LOCUS AR008159 5914 bp DNA PAT 04-DEC-1998

```

DEFINITION Sequence 1 from patent US 5753441.
ACCESSION AR008159
NID 93967268
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5914)
AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Hershan,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.
and Futreal,P. Andrew.
TITLE 170-linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5753441-A 1 19-MAY-1998;
FEATURES
source
1..5914
/organism="unknown"
BASE COUNT 2006 a 1156 c 1316 g 1436 t
ORIGIN

```

```

Query Match 100.0%; Score 5709.4; DB 6; Length 5914;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGGAACCCGACAGGCTGTGGGTTTCTCAGATPACTGGGCC 60
    |||||
Db 1 AGCTGCTGAGACTTCTGGAACCCGACAGGCTGTGGGTTTCTCAGATPACTGGGCC 60
QY 61 CCGGGCTCAGAGAGGCTTCAACCTCTGCTGCTGTTAAAGTTCAATTTGAAGAAAGAA 120
    |||||
Db 61 CCGGGCTCAGAGAGGCTTCAACCTCTGCTGCTGTTAAAGTTCAATTTGAAGAAAGAA 120
QY 121 TGAATTTATCTGCTCTTCCGCTTGAAGAAATGTCATTAATGCTATGAGAA 180
    |||||
Db 121 TGAATTTATCTGCTCTTCCGCTTGAAGAAATGTCATTAATGCTATGAGAA 180
QY 181 TCTTGAAGTGTCCATCTGCTGTGAGTTGATCAAGAACTGTCTCCAGAAAGTGTGACC 240
    |||||
Db 181 TCTTGAAGTGTCCATCTGCTGTGAGTTGATCAAGAACTGTCTCCAGAAAGTGTGACC 240
QY 241 ACATATTTGCAATTTTGCATGCTGGAACCTTCAACCAAGAGGCTTCAACGT 300
    |||||
Db 241 ACATATTTGCAATTTTGCATGCTGGAACCTTCAACCAAGAGGCTTCAACGT 300
QY 301 GTCCCTTATGAAGATGATATTAACCAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360
    |||||
Db 301 GTCCCTTATGAAGATGATATTAACCAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360
QY 361 AACTTGTGAAGAGCTATTTGCAATTTGCTTTTCACTTGCACAGAGTTGGAGT 420
    |||||
Db 361 AACTTGTGAAGAGCTATTTGCAATTTGCTTTTCACTTGCACAGAGTTGGAGT 420
QY 421 ATGCAACAGCTATTAATTTTCAAAAAAGAAATTAATCTCTCTGAAACATTAAGATG 480
    |||||
Db 421 ATGCAACAGCTATTAATTTTCAAAAAAGAAATTAATCTCTCTGAAACATTAAGATG 480
QY 481 AAGTTTCTATCATCAAGATGAGGCTACAGAAACCGTCCAAAGAAAGTCTTACAGAGTG 540
    |||||
Db 481 AAGTTTCTATCATCAAGATGAGGCTACAGAAACCGTCCAAAGAAAGTCTTACAGAGTG 540
QY 541 AACCCGAAATCTTCTCTTGCAGAGAAACAGTCTCAGTGTCAACTCTTAACCTTGGAA 600
    |||||
Db 541 AACCCGAAATCTTCTCTTGCAGAGAAACAGTCTCAGTGTCAACTCTTAACCTTGGAA 600
QY 601 CTGTGAGAACTCTGAGACAAAGAGGAGATACCACTCAAAAGACGCTGTCAATG 660
    |||||
Db 601 CTGTGAGAACTCTGAGACAAAGAGGAGATACCACTCAAAAGACGCTGTCAATG 660
QY 661 AATTGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATGCAAGTGGAG 720
    |||||
Db 661 AATTGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATGCAAGTGGAG 720
QY 721 ATCAAGAAATGTTACAAATCAACCCCTCAAGAACCGAGGATGAATGATTTGATTCG 780
    |||||

```

```
Db 721 ATCAAGATTGTTACAAATCACCCCTCAAGGAACCGGATGAAATCAGTTGGATTTCG 780
Qy 781 CAAAAAGGCGCTGTGTAATTTCTGAGAGGATGTAAACAATCTGAACTCATCAAC 840
Db 781 CAAAAAGGCGCTGTGTAATTTCTGAGAGGATGTAAACAATCTGAACTCATCAAC 840
Qy 841 CCACTAATATGATTTGGAACACCACTGAGAAAGCTGAGAGGATCCAGAAAGT 900
Db 841 CCACTAATATGATTTGGAACACCACTGAGAAAGCTGAGAGGATCCAGAAAGT 900
Qy 901 ATCAGGAGATCTGTTCAAACTGCAATGAGGACATGAGGACCAAAATACTCATGCCA 960
Db 901 ATCAGGAGATCTGTTCAAACTGCAATGAGGACATGAGGACCAAAATACTCATGCCA 960
Qy 961 GCTCATTAACAGATGAGAACAGCAGATTATTACTACTAAGACAGAAATGATGTAGAA 1020
Db 961 GCTCATTAACAGATGAGAACAGCAGATTATTACTACTAAGACAGAAATGATGTAGAA 1020
Qy 1021 AGGCTGAATTCGTAAATTAAGCAAAACAGCCTGCTTAGCAAGAGCCAACTAACAGAT 1080
Db 1021 AGGCTGAATTCGTAAATTAAGCAAAACAGCCTGCTTAGCAAGAGCCAACTAACAGAT 1080
Qy 1081 GGGCTGGAAGTGAAGAAACATGTATAGCGGACTCCCGACAGAAAAAGGTAG 1140
Db 1081 GGGCTGGAAGTGAAGAAACATGTATAGCGGACTCCCGACAGAAAAAGGTAG 1140
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAAAAGATGGAATAGAGAAACTGCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAAAAGATGGAATAGAGAAACTGCCATGCT 1200
Qy 1201 CAGAGAACTCTAGAGATACCTAGATGTTCTTGATTAACACTAAATAGCAGACTTCAGA 1260
Db 1201 CAGAGAACTCTAGAGATACCTAGATGTTCTTGATTAACACTAAATAGCAGACTTCAGA 1260
Qy 1261 AAGTAAATGAGTGGTTTCCAGAAAGTGAAGCTGATGTTAGTTCTGATGCTACATGATG 1320
Db 1261 AAGTAAATGAGTGGTTTCCAGAAAGTGAAGCTGATGTTAGTTCTGATGCTACATGATG 1320
Qy 1321 GGGAGTCTGAATCAAAATCCAAAGTACTGATGTTAGGAGCTTAAATGAGTATG 1380
Db 1321 GGGAGTCTGAATCAAAATCCAAAGTACTGATGTTAGGAGCTTAAATGAGTATG 1380
Qy 1381 AATATTCTGTTCTTCAGAGAAATAGACTTACTGAGGATCTCATGAGGCTTTAA 1440
Db 1381 AATATTCTGTTCTTCAGAGAAATAGACTTACTGAGGATCTCATGAGGCTTTAA 1440
Qy 1441 TATGTAAAGTGAAGAGTACTCTCAATCAGTAGAGATGTAATTTGAAGCAAAATAT 1500
Db 1441 TATGTAAAGTGAAGAGTACTCTCAATCAGTAGAGATGTAATTTGAAGCAAAATAT 1500
Qy 1501 TTGGGAAAACCTATCGGAAGAGGACCTCCCACTTAAGCCATGTAATCTGAAATC 1560
Db 1501 TTGGGAAAACCTATCGGAAGAGGACCTCCCACTTAAGCCATGTAATCTGAAATC 1560
Qy 1561 TAAATTATAGGAGCATTTGTTACTGAGCCAGATATACAGAGGCTCCCTCACAAAATA 1620
Db 1561 TAAATTATAGGAGCATTTGTTACTGAGCCAGATATACAGAGGCTCCCTCACAAAATA 1620
Qy 1621 AATTAAGGCGTAAAGGAGACTACATCAGGCTTCATCCTGAGGATTTTATCAAGAAAG 1680
Db 1621 AATTAAGGCGTAAAGGAGACTACATCAGGCTTCATCCTGAGGATTTTATCAAGAAAG 1680
Qy 1681 CAGATTTGGAGTTCAAAAGAGACTCTGAAATGATTAATCAGGGAATCAACCAAGGAGC 1740
Db 1681 CAGATTTGGAGTTCAAAAGAGACTCTGAAATGATTAATCAGGGAATCAACCAAGGAGC 1740
Qy 1741 AGAATGTCAGATGATTAATTTACTAATAGTGGTCAATGAGATTAACCAAAAGGTGATT 1800
Db 1741 AGAATGTCAGATGATTAATTTACTAATAGTGGTCAATGAGATTAACCAAAAGGTGATT 1800
Qy 1801 CTATTGCAATGAGAAAAATCTAAACCAATAGAAATCACTGAAAAAAGAAATCTGTTCA 1860
Db 1801 CTATTGCAATGAGAAAAATCTAAACCAATAGAAATCACTGAAAAAAGAAATCTGTTCA 1860
Qy 1861 AAACGAAGCTGAACCTTAAGCAGCAGTATTAAGCAATATGAACTGATTAATATCC 1920
Db 1861 AAACGAAGCTGAACCTTAAGCAGCAGTATTAAGCAATATGAACTGATTAATATCC 1920
Qy 1921 ACAATTTAAAAGCACTTAAAAAAGATAGGCTGAGGAGGAAGTCTTACCAAGCATATTC 1980
Db 1921 ACAATTTAAAAGCACTTAAAAAAGATAGGCTGAGGAGGAAGTCTTACCAAGCATATTC 1980
Qy 1981 ATGGCTTGAATCTAGTGTGATGTAATCTAAGCCCACTTAATTTACTGAATTTGAAA 2040
Db 1981 ATGGCTTGAATCTAGTGTGATGTAATCTAAGCCCACTTAATTTACTGAATTTGAAA 2040
Qy 2041 TTGATAGTGTCTTACGAGTGAAGAGATTAAGAAAAAAGTAACTAACCAATGCCAGTCA 2100
Db 2041 TTGATAGTGTCTTACGAGTGAAGAGATTAAGAAAAAAGTAACTAACCAATGCCAGTCA 2100
Qy 2101 GGCACAGCAGAAACCTTACACTCATGGAAGGTAAAGAACTGCATGAGCCAGAGA 2160
Db 2101 GGCACAGCAGAAACCTTACACTCATGGAAGGTAAAGAACTGCATGAGCCAGAGA 2160
Qy 2161 GTAACAGCCAAATGAACAGACAGTAAGACATGACAGCATCTTCCAGAGCTGA 2220
Db 2161 GTAACAGCCAAATGAACAGACAGTAAGACATGACAGCATCTTCCAGAGCTGA 2220
Qy 2221 AGTTAACAAATGCACTGTTCTTTACTAAGTGTTCAAATACAGTGAATTAAGAAAT 2280
Db 2221 AGTTAACAAATGCACTGTTCTTTACTAAGTGTTCAAATACAGTGAATTAAGAAAT 2280
Qy 2281 TTGTCAATCTGACCTTCCAGAGAAAGAAAGAAAGAACTTGAACAGTTAAAGTGT 2340
Db 2281 TTGTCAATCTGACCTTCCAGAGAAAGAAAGAAAGAAAGAACTTGAACAGTTAAAGTGT 2340
Qy 2341 CTAATTAATGCTGAAGACCCCAAGATCATGTTAAATGGAAGAAAGGTTTCAAACTG 2400
Db 2341 CTAATTAATGCTGAAGACCCCAAGATCATGTTAAATGGAAGAAAGGTTTCAAACTG 2400
Qy 2401 AAAGATCTGTAGAGATGACAGTATTTCAATGTTGTTACCTGTTATGAGCAGTCAAG 2460
Db 2401 AAAGATCTGTAGAGATGACAGTATTTCAATGTTGTTACCTGTTATGAGCAGTCAAG 2460
Qy 2461 AAAGATCTGTACTGAGAGTGTGACCTAGGAGAAAGGCAAAACAGAACTTAATAT 2520
Db 2461 AAAGATCTGTACTGAGAGTGTGACCTAGGAGAAAGGCAAAACAGAACTTAATAT 2520
Qy 2521 GTGTAGTCACTGTGACAGCATTTGAAAACCCCAAGGAGTCAATTCAGTGGTTCCAAAG 2580
Db 2521 GTGTAGTCACTGTGACAGCATTTGAAAACCCCAAGGAGTCAATTCAGTGGTTCCAAAG 2580
Qy 2581 ATAAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACACAGTC 2640
Db 2581 ATAAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACACAGTC 2640
Qy 2641 GGGAAACAGCATGGAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700
Db 2641 GGGAAACAGCATGGAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700
Qy 2701 TCAAGGTTTCAAAAGCCGACAGTATTCCTGTTTCCAAATCCAGGAAATGCGAAGAGG 2760
Db 2701 TCAAGGTTTCAAAAGCCGACAGTATTCCTGTTTCCAAATCCAGGAAATGCGAAGAGG 2760
Qy 2761 AATGTGCAACATTCCTGCCCACTCTGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820
Db 2761 AATGTGCAACATTCCTGCCCACTCTGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820
Qy 2821 TTGAATGTGAACAAAGAAAGAAATCAAGGAAAGATGAGTGAATATCAACAGCTGTAC 2880
Db 2821 TTGAATGTGAACAAAGAAAGAAATCAAGGAAAGATGAGTGAATATCAACAGCTGTAC 2880
Qy 2881 AGACAGTTAATATCACTGAGGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940
Db 2881 AGACAGTTAATATCACTGAGGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940
```

QY	2941	ATGCCAAATGTAGTATCAAAAGAGGCTCTAGTGGTTTGTCTATCATCTCAGTTCAAGAGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAAAGAGGAGGCTCTAGTGGTTTGTCTATCATCTCAGTTCAAGAGCA	3000
QY	3001	AGSAACTGAGCATATACCTCCAAATTAACATGCACTTTTACAAAACCATATCGCTATAC	3060
Db	3001	AGSAACTGAGCATATACCTCCAAATTAACATGCACTTTTACAAAACCATATCGCTATAC	3060
QY	3061	CACGACTTTTCCCATCAAGTCATTTGTGTTAAACCTAAATGTAAAGAAAATCGCTAGAGG	3120
Db	3061	CACGACTTTTCCCATCAAGTCATTTGTGTTAAACCTAAATGTAAAGAAAATCGCTAGAGG	3120
QY	3121	AAAACCTTGAGGAACATTCAATGTCACTGACCTGAAAAGAAATGGGAATGGAACATTTCCA	3180
Db	3121	AAAACCTTGAGGAACATTCAATGTCACTGGAAGAAATGGGAATGGAACATTTCCA	3180
QY	3181	GTACAGTAGACACATATAGCCGCTATTAACCTTAGAAGAAATGTTTTTAAGAGAGCCACT	3240
Db	3181	GTACAGTAGACACATATAGCCGCTATTAACCTTAGAAGAAATGTTTTTAAGAGAGCCACT	3240
QY	3241	CAAGCAATATTAAATGAAGTGGTTCCAGTACTATGAGTGGGCTCCAGTATTATTAAGAA	3300
Db	3241	CAAGCAATATTAAATGAAGTGGTTCCAGTACTATGAGTGGGCTCCAGTATTATTAAGAA	3300
QY	3301	TAGGTCCAGTAGAAGAAACATTCACAGCAAACTAGTATGAAAACAGAGGCCAAAATTGA	3360
Db	3301	TAGGTCCAGTAGAAGAAACATTCACAGCAAACTAGTATGAAAACAGAGGCCAAAATTGA	3360
QY	3361	ATGCTATGCTAGATTTAGGGGTTTTGCAACCTGAGTCTATTAACAAAGTCTCTCTGAA	3420
Db	3361	ATGCTATGCTAGATTTAGGGGTTTTGCAACCTGAGTCTATTAACAAAGTCTCTCTGAA	3420
QY	3421	GTAATTGTAAAGCATCTGAAATATAAAAAGCAGAAATATGAAGAGTAGTTGACACTGTTA	3480
Db	3421	GTAATTGTAAAGCATCTGAAATATAAAAAGCAGAAATATGAAGAGTAGTTGACACTGTTA	3480
QY	3481	ATACAGATTTCTCTCCATATCTGATTTCAAGTACTTAAGAAGCCTATNGGAATATCTC	3540
Db	3481	ATACAGATTTCTCTCCATATCTGATTTCAAGTACTTAAGAAGCCTATNGGAATATCTC	3540
QY	3541	ATGCATCTCAGGTTTGTCTGAGACACACTGATGACCTGTAGATGATGGTGAAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTCTGAGACACACTGATGACCTGTAGATGATGGTGAAATTAAGG	3600
QY	3601	AAAGTACTAGTTTGTCTGAAATATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAACCG	3660
Db	3601	AAAGTACTAGTTTGTCTGAAATATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAACCG	3660
QY	3661	TCCGAAGAAGGAGACTTAGACAGAGAGTCTAGGCCCTTCCACCATACAAATTTGGCTCAGG	3720
Db	3661	TCCGAAGAAGGAGACTTAGACAGAGAGTCTAGGCCCTTCCACCATACAAATTTGGCTCAGG	3720
QY	3721	GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAGAAGAACTTATCTAGTGGAGATG	3780
Db	3721	GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAGAAGAACTTATCTAGTGGAGATG	3780
QY	3781	AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAATGAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAATGAATATACCTTCTCAGT	3840
QY	3841	CTATATAGCATAGACCGCTGTACACGAGAGTGTGCTTAAGAACACAGAGGAGAAATTAT	3900
Db	3841	CTATATAGCATAGACCGCTGTACACGAGAGTGTGCTTAAGAACACAGAGGAGAAATTAT	3900
QY	3901	TATCATTTGAAGATAGCTTAAATGACTGCAGTACACGAGTAATATTGGCAAGGCATCTC	3960
Db	3901	TATCATTTGAAGATAGCTTAAATGACTGCAGTACACGAGTAATATTGGCAAGGCATCTC	3960
QY	3961	AGGAACATCACCTTAGTAGAGGAAACAAAATGTCTGCTAGCTGTTGTTCTTCCACAGTGCA	4020
Db	3961	AGGAACATCACCTTAGTAGAGGAAACAAAATGTCTGCTAGCTGTTGTTCTTCCACAGTGCA	4020

QY	4021	GTGAATTGGGAAGACTTGCATCTGCAAAATTCAAATCCACCAGATCCTTCTTGATGGTCTT	4088
Db	4021	GTGAATTGGGAAGACTTGCATCTGCAAAATTCAAATCCACCAGATCCTTCTTGATGGTCTT	4080
QY	4081	CCAAACCAATAGGCATTCAGTCTGAAAGCCAGGAGTTGTCGAGTGCACAGAAATGG	4140
Db	4081	CCAAACCAATAGGCATTCAGTCTGAAAGCCAGGAGTTGTCGAGTGCACAGAAATGG	4140
QY	4141	TTTCAGATGATGAAGAAAGGAAGCGGGCTTGGAAAGAAATATCAAGAAAGCAAAACA	4200
Db	4141	TTTCAGATGATGAAGAAAGGAAGCGGGCTTGGAAAGAAATATCAAGAAAGCAAAACA	4200
QY	4201	TGGATTCAAACCTTGTGGGAAGCAGCATCTGGTGTGAGAGTGAACAGCCTCTTGAG	4266
Db	4201	TGGATTCAAACCTTGTGGGAAGCAGCATCTGGTGTGAGAGTGAACAGCCTCTTGAG	4266
QY	4261	ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAACACTCAGACAGAGGGTATCAATGC	4320
Db	4261	ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAACACTCAGACAGAGGGTATCAATGC	4320
QY	4321	AACATTAACCTGATATTAAGCTCCAGCAGAGAAATGGCTCAACATAGAGCTGTGTAGAAGC	4386
Db	4321	AACATTAACCTGATATTAAGCTCCAGCAGAGAAATGGCTCAACATAGAGCTGTGTAGAAGC	4386
QY	4381	ATGGAGAGCAGCCTCTTCAACAGCTACCCCTTCATCAATAGACCTCTTCCCTTGAGG	4440
Db	4381	ATGGAGAGCAGCCTCTTCAACAGCTACCCCTTCATCAATAGACCTCTTCCCTTGAGG	4440
QY	4441	ACCTGCGAAATCCGAAACAAAGCAATCAGAAAAACGATATTAACTTCACGAAAACTA	4500
Db	4441	ACCTGCGAAATCCGAAACAAAGCAATCAGAAAAACGATATTAACTTCACGAAAACTA	4500
QY	4501	GTGAATACCCATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTGGAGTGTG	4566
Db	4501	GTGAATACCCATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTGGAGTGTG	4566
QY	4561	CAGATAGTTCTACCAAGTAAAAATTAAGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT	4620
Db	4561	CAGATAGTTCTACCAAGTAAAAATTAAGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT	4620
QY	4621	GCCCATCTTATTAAGATTAAGGTGTACATGCACAGTTGCTCTGGAGTCTTCAGAAATATA	4686
Db	4621	GCCCATCTTATTAAGATTAAGGTGTACATGCACAGTTGCTCTGGAGTCTTCAGAAATATA	4686
QY	4681	ACTACCCATCTCAAGAGAGACTCATTAAGGTTTGTATGTGAGAGGCAACAGCTGGAG	4740
Db	4681	ACTACCCATCTCAAGAGAGACTCATTAAGGTTTGTATGTGAGAGGCAACAGCTGGAG	4740
QY	4741	AGTGTGGGCCACAGATTTGACGGAACAATCTTACTTGGCAAGGCAAGATCTAGAGGAA	4800
Db	4741	AGTGTGGGCCACAGATTTGACGGAACAATCTTACTTGGCAAGGCAAGATCTAGAGGAA	4800
QY	4801	CCCCCTACCTGGAATCTGGAATACGCCCTTCTCTGATGACCCCTGAATCTGATCCTCTG	4860
Db	4801	CCCCCTACCTGGAATCTGGAATACGCCCTTCTCTGATGACCCCTGAATCTGATCCTCTG	4860
QY	4861	AAGACAGAGCCCAAGATCTAGCTCGGTGGGCAACAATACCATCTCAACCTCTGATATGA	4920
Db	4861	AAGACAGAGCCCAAGATCTAGCTCGGTGGGCAACAATACCATCTCAACCTCTGATATGA	4920
QY	4921	AAGTTCGCCCAATTAAGTTGACAGATCTGCCAGAGTCCACCTGCTCTATACTACTG	4980
Db	4921	AAGTTCGCCCAATTAAGTTGACAGATCTGCCAGAGTCCACCTGCTCTATACTACTG	4980
QY	4981	ATACCTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAAAGCAAAATGTGACAG	5040
Db	4981	ATACCTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAAAGCAAAATGTGACAG	5040
QY	5041	CTTCAACAGAAAGGCTCAACAAAAGAAATCCATGCTGTGCTGCTGACCCCAAGAG	5100
Db	5041	CTTCAACAGAAAGGCTCAACAAAAGAAATCCATGCTGTGCTGCTGACCCCAAGAG	5100
QY	5101	AATTATAGCTCTGTATCAACCTTTGGCCAGAAAAACACCATCTCACTTAACTATCTAATTA	5160







QY 1141 ATCTGATGCTGATCCCTGCTGTGAGAGAAAAGATGGAATAGCAGAACTGCCATCT 1200  
 Db 1141 ATCTGATGCTGATCCCTGCTGTGAGAGAAAAGATGGAATAGCAGAACTGCCATCT 1200  
 QY 1201 CAGAGAACTCTAGAGATCTAGATGCTTCTTGATTAACATAATAGCAGATTCAGA 1260  
 Db 1201 CAGAGAACTCTAGAGATCTAGATGCTTCTTGATTAACATAATAGCAGATTCAGA 1260  
 QY 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAACGTGTAGTTCTGATGACTCAGATGATG 1320  
 Db 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAACGTGTAGTTCTGATGACTCAGATGATG 1320  
 QY 1321 GGGAGTCTGATCAAAATCCCAAGTGTGATGTTTGGAGCTTAAATAGAGTATG 1380  
 Db 1321 GGGAGTCTGATCAAAATCCCAAGTGTGATGTTTGGAGCTTAAATAGAGTATG 1380  
 QY 1381 AATATTCGTCTCTCAGAGAAAATAGACTTACTGCGCAGTATCCTCATGAGCTTTAA 1440  
 Db 1381 AATATTCGTCTCTCAGAGAAAATAGACTTACTGCGCAGTATCCTCATGAGCTTTAA 1440  
 QY 1441 TATGTAAAGTGAAGAGTCTCACTCCAAATCAGTAGAGATATATTTGAGACAAAATAT 1500  
 Db 1441 TATGTAAAGTGAAGAGTCTCACTCCAAATCAGTAGAGATATATTTGAGACAAAATAT 1500  
 QY 1501 TTGGGAAAACCTATCGGAGAAAGGCAAGCCTCCCACTTAAGCCATGTAAGTAAATC 1560  
 Db 1501 TTGGGAAAACCTATCGGAGAAAGGCAAGCCTCCCACTTAAGCCATGTAAGTAAATC 1560  
 QY 1561 TAAATATAGAGACATTTTGTACTGAGCAGACAGATATATCAAGAGGTCCTCCACAAATA 1620  
 Db 1561 TAAATATAGAGACATTTTGTACTGAGCAGACAGATATATCAAGAGGTCCTCCACAAATA 1620  
 QY 1621 AATTTAAAGCGTAAAGAGAGACCTACATGAGCCTTCACTGAGATTTTATCAAGAAAG 1680  
 Db 1621 AATTTAAAGCGTAAAGAGAGAGACCTACATGAGCCTTCACTGAGATTTTATCAAGAAAG 1680  
 QY 1681 CAGATTTGGGAGTTCAAAGAGACCTCTGAAATGATTAATCAGGAAACCTAACCAAGGAGC 1740  
 Db 1681 CAGATTTGGGAGTTCAAAGAGACCTCTGAAATGATTAATCAGGAAACCTAACCAAGGAGC 1740  
 QY 1741 AGAATGCTCAAGTATGATATTTACTAATAGTGTGATGATGAAATTAACAAAGGATGAT 1800  
 Db 1741 AGAATGCTCAAGTATGATATTTACTAATAGTGTGATGATGAAATTAACAAAGGATGAT 1800  
 QY 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAATCTGCTTCA 1860  
 Db 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAATCTGCTTCA 1860  
 QY 1861 AAAGGAAAGCTGAACTTAAGCAGCAGATATAGCAATATGGAATCGAATTTAATATCC 1920  
 Db 1861 AAAGGAAAGCTGAACTTAAGCAGCAGATATAGCAATATGGAATCGAATTTAATATCC 1920  
 QY 1921 ACAATTCAAAAGACCTTAAAGAAATAGCTGAGAGAGAACTCTTCTACAGCAGATATTC 1980  
 Db 1921 ACAATTCAAAAGACCTTAAAGAAATAGCTGAGAGAGAACTCTTCTACAGCAGATATTC 1980  
 QY 1981 ATGCGCTTGAACCTAGTACTGATGAAATCTTAAGCCCACTAATTTGTAAGTAAATGCAAA 2040  
 Db 1981 ATGCGCTTGAACCTAGTACTGATGAAATCTTAAGCCCACTAATTTGTAAGTAAATGCAAA 2040  
 QY 2041 TTGATAGTGTCTAGCAGTGAAGATTAAGAAAAAATATACAACTAATTTGCAAGTCA 2100  
 Db 2041 TTGATAGTGTCTAGCAGTGAAGATTAAGAAAAAATATACAACTAATTTGCAAGTCA 2100  
 QY 2101 GGCACAGAGAAACCTTACAACTCATGAAAGTAAAGAACTGCAAACTGAGAACCAAGAGA 2160  
 Db 2101 GGCACAGAGAAACCTTACAACTCATGAAAGTAAAGAACTGCAAACTGAGAACCAAGAGA 2160  
 QY 2161 GTAACAGACCAATGACAGACAAAGTAAAGACATGACAGGATATCTTCCAGAGCTGA 2220  
 Db 2161 GTAACAGACCAATGACAGACAAAGTAAAGACATGACAGGATATCTTCCAGAGCTGA 2220  
 QY 2221 AGTTAACAAATGACACCTGCTTTTACTAAGTGTTCAAATACCAAGTAACTTAAGAT 2280

Db 2221 AGTTAACAAATGACACCTGCTTTTACTAAGTGTTCAAATACCAAGTAACTTAAGAT 2280  
 QY 2281 TTGTCAATCTTACGCTTCCAAAGAGAGAAAAAGAGAAAATAGAAAACAGTTAAAGT 2340  
 Db 2281 TTGTCAATCTTACGCTTCCAAAGAGAGAAAAAGAGAAAATAGAAAACAGTTAAAGT 2340  
 QY 2341 CTAATATGCTGAAGAGCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCNAAGT 2400  
 Db 2341 CTAATATGCTGAAGAGCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCNAAGT 2400  
 QY 2401 AAAGATCTGAGAGATGAGCATTTTCAATGTTGTAACCGTACCTGATTAAGGCACTCAG 2460  
 Db 2401 AAAGATCTGAGAGATGAGCATTTTCAATGTTGTAACCGTACCTGATTAAGGCACTCAG 2460  
 QY 2461 AAAGATCTGAGAGATGAGCATTTTCAATGTTGTAACCGTACCTGATTAAGGCACTCAG 2520  
 Db 2461 AAAGATCTGAGAGATGAGCATTTTCAATGTTGTAACCGTACCTGATTAAGGCACTCAG 2520  
 QY 2521 GTGTGAGTCAAGTGTGACAGCATTTGAAAAACCCCAAGGACATATTCATGTTGTTCCAAAG 2580  
 Db 2521 GTGTGAGTCAAGTGTGACAGCATTTGAAAAACCCCAAGGACATATTCATGTTGTTCCAAAG 2580  
 QY 2581 AATAATGAAATGACACAGAGGCTTTAAGTATCCATGGGACATGAGTTAACCAAGTCC 2640  
 Db 2581 AATAATGAAATGACACAGAGGCTTTAAGTATCCATGGGACATGAGTTAACCAAGTCC 2640  
 QY 2641 GGGAAACAGCATAGAAATGAGAAAGAGTGAATGCTCAGTATTTGCGAATACAT 2700  
 Db 2641 GGGAAACAGCATAGAAATGAGAAAGAGTGAATGCTCAGTATTTGCGAATACAT 2700  
 QY 2701 TCAAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCCAGAAATGAGAGAGG 2760  
 Db 2701 TCAAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCCAGAAATGAGAGAGG 2760  
 QY 2761 AATGTGCAACATTTCTGCGCCACTCTGGGCTTAAAGAAACCAAGTCCAAAGTCACTT 2820  
 Db 2761 AATGTGCAACATTTCTGCGCCACTCTGGGCTTAAAGAAACCAAGTCCAAAGTCACTT 2820  
 QY 2821 TTGATGATGAAACAAAGAGAGAAATATCAGGAAAGATGATGATATATCAAGCTGTAC 2880  
 Db 2821 TTGATGATGAAACAAAGAGAGAAATATCAGGAAAGATGATGATATATCAAGCTGTAC 2880  
 QY 2881 AGACAGTTAATATCACTGACAGGCTTCTGCTGTGTTGCTCAGAAAGATPAGCCAGTGTATA 2940  
 Db 2881 AGACAGTTAATATCACTGACAGGCTTCTGCTGTGTTGCTCAGAAAGATPAGCCAGTGTATA 2940  
 QY 2941 ATGCGAAATGAGTAAAGAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGACA 3000  
 Db 2941 ATGCGAAATGAGTAAAGAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGACA 3000  
 QY 3001 ACGAAATCTGACACTATTAATCTCAATTAACATGAGACTTTTCAAAACCCATATGTAATC 3060  
 Db 3001 ACGAAATCTGACACTATTAATCTCAATTAACATGAGACTTTTCAAAACCCATATGTAATC 3060  
 QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAGAAAAATCTGTAAGG 3120  
 Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAGAAAAATCTGTAAGG 3120  
 QY 3121 AAAACTTTGAGAGAACTTCAATGTCACCTGAAAAGAGAAATGAGAAATGAGAACTTCCAA 3180  
 Db 3121 AAAACTTTGAGAGAACTTCAATGTCACCTGAAAAGAGAAATGAGAAATGAGAACTTCCAA 3180  
 QY 3181 GTACAGTGAAGACAAATAGCCGTATTAACATATTAAGAAAAATGTTTAAAGAACCCAGCT 3240  
 Db 3181 GTACAGTGAAGACAAATAGCCGTATTAACATATTAAGAAAAATGTTTAAAGAACCCAGCT 3240  
 QY 3241 CAAAGCAATATTAATGAGAGTGTCCAGTACTAATGAAGTGGGCTCCAGATTAATGAAGA 3300  
 Db 3241 CAAAGCAATATTAATGAGAGTGTCCAGTACTAATGAAGTGGGCTCCAGATTAATGAAGA 3300  
 QY 3301 TAGGTTCCAGGATGAGAAACATTCACAGACAACTAGTAAACAGAGGCGCAAAATGA 3360

QY	4441	ACCTGCCAATTCGAAACGAAGCAATCGAGAAACGATATTAATCTACAGAAAGTA	4500
Db	4441	ACCTGCCAATTCGAAACGAAGCAATCGAGAAACGATATTAATCTACAGAAAGTA	4500
QY	4501	GTGAAATACCCATATAGCCAGAAATCCAGAAAGCCCTTCTCTACAAAGTTTGAGTGTCTG	4560
Db	4501	GTGAAATACCCATATAGCCAGAAATCCAGAAAGCCCTTCTCTACAAAGTTTGAGTGTCTG	4560
QY	4551	CAGATAGTTCTACCAAGTAAAAATAAAGAACCAAGAGTGAAGAAAGTCATCCCTTTAAAT	4620
Db	4551	CAGATAGTTCTACCAAGTAAAAATAAAGAACCAAGAGTGAAGAAAGTCATCCCTTTAAAT	4620
QY	4621	GCCCATCATTAAGATGATAGGTGGTACATGCACAGTTGCTCTGGAGTCTTCGAATAGAA	4680
Db	4621	GCCCATCATTAAGATGATAGGTGGTACATGCACAGTTGCTCTGGAGTCTTCGAATAGAA	4680
QY	4681	ACTACCATCTCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGCAACAGCTGGAG	4740
Db	4681	ACTACCATCTCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGCAACAGCTGGAG	4740
QY	4741	AGCTGGGGCCACAGATTGACGGAACAATCTTACTTGCAGAGCAAGATCTAGAGGAA	4800
Db	4741	AGCTGGGGCCACAGATTGACGGAACAATCTTACTTGCAGAGCAAGATCTAGAGGAA	4800
QY	4801	CCCCCTTACCTGGAATCTGGAATCAGCCCTCTTCTGATGACCCCTGAATCTGATCTCTG	4860
Db	4801	CCCCCTTACCTGGAATCTGGAATCAGCCCTCTTCTGATGACCCCTGAATCTGATCTCTG	4860
QY	4861	AAGACAGAGCCCGAGAGTCAAGTCTGTGTTGGCAACATACCATCTTCAACCTGTGATTGA	4920
Db	4861	AAGACAGAGCCCGAGAGTCAAGTCTGTGTTGGCAACATACCATCTTCAACCTGTGATTGA	4920
QY	4921	AAGTTCCTCCATTTGAAAGTTCGAGATCTGCCAGAGTCCACCTCTGCTCATACTACTG	4980
Db	4921	AAGTTCCTCCATTTGAAAGTTCGAGATCTGCCAGAGTCCACCTCTGCTCATACTACTG	4980
QY	4981	ATATCTGCTGGATATATGCAATGGAAGAAAGTGTGAGCAGGGAGAAAGCCAGATTGACAG	5040
Db	4981	ATATCTGCTGGATATATGCAATGGAAGAAAGTGTGAGCAGGGAGAAAGCCAGATTGACAG	5040
QY	5041	CTTCAACAGAAAGGCTCAACAAAAAGAAATCCATGGTGGTCTGAGCCGACCCAGAG	5100
Db	5041	CTTCAACAGAAAGGCTCAACAAAAAGAAATCCATGGTGGTCTGAGCCGACCCAGAG	5100
QY	5101	AATTTATGCTCGTGTACAAAGTTGCCAGAAACACACATCACTTAACTAATCAATTA	5160
Db	5101	AATTTATGCTCGTGTACAAAGTTGCCAGAAACACACATCACTTAACTAATCAATTA	5160
QY	5161	CTGAAAGAGATCTACTGTTGTTATATAAAAAAGATGCTGATGTGTGAACGGAGAC	5220
Db	5161	CTGAAAGAGATCTACTGTTGTTATATAAAAAAGATGCTGATGTGTGAACGGAGAC	5220
QY	5221	TGAATAATTTTCTAGAGAAATGCGGAGAGAAATGGTATGATTTCTGGGTGACCC	5280
Db	5221	TGAATAATTTTCTAGAGAAATGCGGAGAGAAATGGTATGATTTCTGGGTGACCC	5280
QY	5281	AGTCTATTTAAAGAAAGAAAATGCTGATGACATGATTTTGAAGTCAAGAGAGATGG	5340
Db	5281	AGTCTATTTAAAGAAAGAAAATGCTGATGACATGATTTTGAAGTCAAGAGAGATGG	5340
QY	5341	TCAATGGAAGAAACCAACAAAGGTCGAAAGCGAGCAAGAAATCCAGAGACAGAAAAGTCT	5400
Db	5341	TCAATGGAAGAAACCAACAAAGGTCGAAAGCGAGCAAGAAATCCAGAGACAGAAAAGTCT	5400
QY	5401	TCAAGGGGGCTAGAAATCTGTGTGTATGGCCCTTCCACAACTATGCCCACAGATCAACTGG	5460
Db	5401	TCAAGGGGGCTAGAAATCTGTGTGTATGGCCCTTCCACAACTATGCCCACAGATCAACTGG	5460
QY	5461	AATGGAATGATACAGCTGTGTGTGTCTTCTGTGTGTGAAGAGCTTTCATCATTTACACCTTG	5520
Db	5461	AATGGAATGATACAGCTGTGTGTGTCTTCTGTGTGTGAAGAGCTTTCATCATTTACACCTTG	5520

OY	5521	GCACAGGTTCCACCAATGTGGTTGTGCACACAGATGCTCGGACAGAGGACCAATGGCT	5580
Db	5521	GCACAGGTTCCACCAATGTGGTTGTGCACACAGATGCTCGGACAGAGGACCAATGGCT	5580
OY	5581	TCCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGGACA	5640
Db	5581	TCCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGGACA	5640
OY	5641	GTGTAGACACTTACACAGTGCACAGAGCTGGACCTACCTGATATACCCAGATCCCCACA	5700
Db	5641	GTGTAGACACTTACACAGTGCACAGAGCTGGACCTACCTGATATACCCAGATCCCCACA	5700
OY	5701	GGCACTACTGA 5711	
Db	5701	GGCACTACTGA 5711	
RESULT	5		
LOCUS	180938	180938 5914 bp DNA	PAT 20-MAR-1998
DEFINITION	Sequence 1 from patent US 5709999.		
ACCESSION	180938		
NID	93209228		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 5914)		
	Shattuck-Baldens,D.M., Simard,J., Durocher,F., Eml,M. and Nakamura,Y.		
TITLE	Linked breast and ovarian cancer susceptibility gene		
JOURNAL	Patent: US 5709999-A 1 20-JAN-1998;		
FEATURES	Location/Qualifiers		
Source	1..5914		
	/organism="unknown"		
BASE COUNT	2006 a 1156 c 1316 g 1436 t		
ORIGIN			
Query Match	100.0%; Score 5709.4; DB 6; Length 5914;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 5710: Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
OY	1	AGCTGCGTGAGACTTCCTGGAGACCCGCGACACAGGCTGTGGGTTTTCAGATTAAGTGGCC	60
Db	1	AGCTGCGTGAGACTTCCTGGAGACCCGCGACACAGGCTGTGGGTTTTCAGATTAAGTGGCC	60
OY	61	CCTGGCGTCAGAGGCGCTTACCTCTGCTGTGGGTTAAAGTTCATTGGACGAAAGAA	120
Db	61	CCTGGCGTCAGAGGCGCTTACCTCTGCTGTGGGTTAAAGTTCATTGGACGAAAGAA	120
OY	121	TGGATTATCTGCTCTTGGCGCTTGAAGAAGTACAAAAATGCTAATGCTATGACAGAAA	180
Db	121	TGGATTATCTGCTCTTGGCGCTTGAAGAAGTACAAAAATGCTAATGCTATGACAGAAA	180
OY	181	TCTTGAAGTGTCCATCTGTCTGTGAAGTTGATCAAGAACCTGTCTCCAAAGTGTGACC	240
Db	181	TCTTGAAGTGTCCATCTGTCTGTGAAGTTGATCAAGAACCTGTCTCCAAAGTGTGACC	240
OY	241	ACATATTTTGGCAAAATTTGGCATGCGAAACTCTCAACCGAAGAAAGGCGCTTGACACT	300
Db	241	ACATATTTTGGCAAAATTTGGCATGCGAAACTCTCAACCGAAGAAAGGCGCTTGACACT	300
OY	301	GTCCTTATGTAGATATATATACCAAAAGGAGCTACAAAGAAATGAGATTTAGTC	360
Db	301	GTCCTTATGTAGATATATATACCAAAAGGAGCTACAAAGAAATGAGATTTAGTC	360
OY	361	AACTGTTGAGAGAGCTATTTGAAATCATTTGTGCTTTTCAGCTTGACACAGGTTGGAGT	420
Db	361	AACTGTTGAGAGAGCTATTTGAAATCATTTGTGCTTTTCAGCTTGACACAGGTTGGAGT	420
OY	421	ATGCAAAAGCTATATTTTGGAAAAAGGAAATTAACCTCTCTGACATCTTAAAGATG	480

D	421	ATGC	AACG	CGTAT	TAAT	TTTGG	CAAAAA	AGSAA	TA	TAC	TCT	CTG	AAC	TCT	TA	CA	CT	TA	CA	AA	GA	AG	TG	480										
Q	481	AA	GT	T	C	A	T	C	A	T	C	C	A	A	A	G	T	A	G	G	G	C	T	C	A	G	A	G	T	G	540			
D	481	AA	GT	T	C	A	T	C	A	T	C	C	A	A	A	G	T	A	G	G	G	C	T	C	A	G	A	G	T	G	540			
Q	541	AA	CC	G	A	A	A	A	A	C	T	T	C	C	T	T	C	C	A	G	A	A	A	A	A	A	A	A	A	A	A	600		
D	541	AA	CC	G	A	A	A	A	A	C	T	T	C	C	T	T	C	C	A	G	A	A	A	A	A	A	A	A	A	A	A	600		
Q	601	C	T	G	T	G	A	A	C	T	C	T	G	A	G	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	660		
D	601	C	T	G	T	G	A	A	C	T	C	T	G	A	G	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	660		
Q	661	AA	T	T	G	G	A	T	C	G	A	T	T	C	T	G	A	A	G	A	T	A	A	A	A	A	A	A	A	A	A	720		
D	661	AA	T	T	G	G	A	T	C	G	A	T	T	C	T	G	A	A	G	A	T	A	A	A	A	A	A	A	A	A	A	720		
Q	721	AT	CA	GA	AT	T	G	T	CA	AA	T	CA	CC	C	C	T	C	A	G	A	A	CC	A	G	G	A	T	GA	AT	T	G	780		
D	721	AT	CA	GA	AT	T	G	T	CA	AA	T	CA	CC	C	C	T	C	A	G	A	A	CC	A	G	G	A	T	GA	AT	T	G	780		
Q	781	CA	AA	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	840		
D	781	CA	AA	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	840		
Q	841	CC	AG	TA	AT	A	T	A	T	A	G	TT	G	A	AC	CA	CT	G	A	GA	AG	CG	T	G	AG	AG	CC	T	CA	GA	AA	AG	900	
D	841	CC	AG	TA	AT	A	T	A	T	A	G	TT	G	A	AC	CA	CT	G	A	GA	AG	CG	T	G	AG	AG	CC	T	CA	GA	AA	AG	900	
Q	901	AT	CA	GG	GA	AT	T	C	T	G	T	CA	AA	T	C	T	G	A	T	G	A	G	C	A	T	G	G	C	A	A	A	T	960	
D	901	AT	CA	GG	GA	AT	T	C	T	G	T	CA	AA	T	C	T	G	A	T	G	A	G	C	A	T	G	G	C	A	A	A	T	960	
Q	961	G	C	T	A	T	T	A	C	A	C	A	T	G	A	C	A	G	A	G	C	A	G	A	G	C	A	G	A	G	C	A	1020	
D	961	G	C	T	A	T	T	A	C	A	C	A	T	G	A	C	A	G	A	G	C	A	G	A	G	C	A	G	A	G	C	A	1020	
Q	1021	AG	G	C	T	A	T	T	C	T	G	T	CA	AA	A	G	CA	AG	C	T	G	T	T	A	C	CA	GA	GA	GC	CA	CA	T	1080	
D	1021	AG	G	C	T	A	T	T	C	T	G	T	CA	AA	A	G	CA	AG	C	T	G	T	T	A	C	CA	GA	GA	GC	CA	CA	T	1080	
Q	1081	G	G	G	C	T	G	A	A	G	A	T	A	G	A	A	C	A	T	G	A	T	A	G	C	C	C	A	C	A	A	A	A	1140
D	1081	G	G	G	C	T	G	A	A	G	A	T	A	G	A</																			

OY	2641	GGGAAACAGCATGGAATGGAAGAAAGTAAGTACCTGATGTCGTGCTTTGGCAAGTATAC	2700
Db	2641	GCGAAACAGCATGGAATGGAAGAAAGTAACTTGTATGCTCATGTTTGGCAAGTATAC	2700
OY	2701	TCAAAGTTTCAAAGCGCCAGTCATTTCCTGTGTTTCAAATCCAGGAAATGCAGAGAGG	2760
Db	2641	GCGAAACAGCATGGAATGGAAGAAAGTAACTTGTATGCTCATGTTTGGCAAGTATAC	2700
OY	2701	TCAAAGTTTCAAAGCGCCAGTCATTTCCTGTGTTTCAAATCCAGGAAATGCAGAGAGG	2760
Db	2701	TCAAAGTTTCAAAGCGCCAGTCATTTCCTGTGTTTCAAATCCAGGAAATGCAGAGAGG	2760
OY	2761	AATGCGAAACCTTCCTGCGCCACCTCGGGGTCCTTAAAGAAACCAAAAGTCCAAAGTCACCT	2820
Db	2761	AATGCGAAACCTTCCTGCGCCACCTCGGGGTCCTTAAAGAAACCAAAAGTCCAAAGTCACCT	2820
OY	2821	TTGAATGTGAACAAAGAGAGAAAAATCAAGAAAGAAATGAGTCTAATATCAAGCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAGAGAGAAAAATCAAGAAAGAAATGAGTCTAATATCAAGCCTGTAC	2880
OY	2881	AGACAGTTAAATATCATCTGCGAGCGCTTCCTCTGCTGGTGTCAAGAAAGATAGCCAGTTGATA	2940
Db	2881	AGACAGTTAAATATCATCTGCGAGCGCTTCCTCTGCTGGTGTCAAGAAAGATAGCCAGTTGATA	2940
OY	2941	ATGCCAAATGTAGTATCAAAAGAGAGGCTCTAGTGTGTTGTCATCATCTCAGTTCAGAGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAAAGAGAGGCTCTAGTGTGTTGTCATCATCTCAGTTCAGAGCA	3000
OY	3001	ACGAAACTGGACTCATTTACTCCAAATTAACATGAGCTTTTACAAAACCCATATGCTATAC	3060
Db	3001	ACGAAACTGGACTCATTTACTCCAAATTAACATGAGCTTTTACAAAACCCATATGCTATAC	3060
OY	3061	CACACATTTTCCCATCAATCATATTTGTTTAAACTAAATGTAAAGAAAATATCGATAGAGG	3120
Db	3061	CACACATTTTCCCATCAATCATATTTGTTTAAACTAAATGTAAAGAAAATATCGATAGAGG	3120
OY	3121	AAAACTTTGAGGAACATTTCATGTCACCTGTAAGAGAAATGGGAATGAGAACATTTCGA	3180
Db	3121	AAAACTTTGAGGAACATTTCATGTCACCTGTAAGAGAAATGGGAATGAGAACATTTCGA	3180
OY	3181	GTCANGTGAGACAAATTAGCCGTTAATTAACATTAGAGAAAAATGTTTTTAAAGAGCCACT	3240
Db	3181	GTCANGTGAGACAAATTAGCCGTTAATTAACATTAGAGAAAAATGTTTTTAAAGAGCCACT	3240
OY	3241	CAACCAATATTAATGAAGTGTGTTCCAGTACTAATGAGTGGGCTCCAGTATTAATGAAA	3300
Db	3241	CAACCAATATTAATGAAGTGTGTTCCAGTACTAATGAGTGGGCTCCAGTATTAATGAAA	3300
OY	3301	TAGTTCACAGTGAATGAACATCTCAACGAGACTAGTGTGAAAACAGAGGCCCAAAATTTGA	3360
Db	3301	TAGTTCACAGTGAATGAACATCTCAACGAGACTAGTGTGAAAACAGAGGCCCAAAATTTGA	3360
OY	3361	ATGCTATGCTAGATTTAGGGGTTTGGCAACCTAGGTCTATTAACAAAGTCTTCTCTGAAA	3420
Db	3361	ATGCTATGCTAGATTTAGGGGTTTGGCAACCTAGGTCTATTAACAAAGTCTTCTCTGAAA	3420
OY	3421	GTAATTTGTAAAGCATCTGGAATTAATAAAGCAGAATATGAGAAGTACTGACACTGTTA	3480
Db	3421	GTAATTTGTAAAGCATCTGGAATTAATAAAGCAGAATATGAGAAGTACTGACACTGTTA	3480
OY	3481	ATAAGATTTCTCTCCATATCTGATTTTCAGATTAACATAAGCCATATGGGAATGATC	3540
Db	3481	ATAAGATTTCTCTCCATATCTGATTTTCAGATTAACATAAGCCATATGGGAATGATC	3540
OY	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATAGACCTGTAGATGATGCGTGAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATAGACCTGTAGATGATGCGTGAATTAAGG	3600
OY	3601	AAGATTAAGTGTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTTAAAGCAAAACCG	3660
Db	3601	AAGATTAAGTGTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTTAAAGCAAAACCG	3660
OY	3661	TCCAGAAAGAGAGGCTTAGAGAGAGTCTAGAGCCCTTTCACCCATACAAATTTGGCTCAGG	3720
Db	3661	TCCAGAAAGAGAGGCTTAGAGAGAGTCTAGAGCCCTTTCACCCATACAAATTTGGCTCAGG	3720
OY	3721	GTTTACCAGAGGGGCCAAGAAATTTAGAGTCTCTCAGAAAGAGAACTTATCTAGTGGAGAT	3780

|||||  
Db 3721 GTTACCGAAGGGGCGCAGAAATTAAGTCTCTAGAAAGAACTTATCTAGTAGAGTG 3780  
QY 3781 AAGAGCTTCCCTGGTCCACACTTGTATTTGGTAAAGTAAACATATACCTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGGTCCACACTTGTATTTGGTAAAGTAAACATATACCTCTCAGT 3840  
QY 3841 CTACTAGGCATAGACCGTGTCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGACCGTGTCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900  
QY 3901 TATATTGAAGAAATAGCTTAATAGTCACTAACCAGTAAATTTGGCAAGGACATCTC 3960  
Db 3901 TATATTGAAGAAATAGCTTAATAGTCACTAACCAGTAAATTTGGCAAGGACATCTC 3960  
QY 3961 AGAACAATCACCCTTAGTAGAGGAAACAAATGTCTGTAGCTTTCTTCTCAGAGTCA 4020  
Db 3961 AGAACAATCACCCTTAGTAGAGGAAACAAATGTCTGTAGCTTTCTTCTCAGAGTCA 4020  
QY 4021 GTGAATTTGGAAGACTTGTGACTCAAAATACAAACACCCAGAGATCTTTCTGTATGTTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGTGACTCAAAATACAAACACCCAGAGATCTTTCTGTATGTTCTT 4080  
QY 4081 CCAACAAATAGGAGCATCAGTCTGAAGCCAGGAGTTGGTGTAGTACAGCAAGAAATGG 4140  
Db 4081 CCAACAAATAGGAGCATCAGTCTGAAGCCAGGAGTTGGTGTAGTACAGCAAGAAATGG 4140  
QY 4141 TTTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATCAAGAAAGCAAGCA 4200  
Db 4141 TTTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATCAAGAAAGCAAGCA 4200  
QY 4201 TGGATTCAAACTTAGTGAAGACAGCATCTGGGTGTAGAGTGAACAACGCTCTCTGAAG 4260  
Db 4201 TGGATTCAAACTTAGTGAAGACAGCATCTGGGTGTAGAGTGAACAACGCTCTCTGAAG 4260  
QY 4261 ACTGCTAGGGGCTTCTCTCAGAGTACATTTTAAACACTCAGCAGAGAGATACCATGC 4320  
Db 4261 ACTGCTAGGGGCTTCTCTCAGAGTACATTTTAAACACTCAGCAGAGAGATACCATGC 4320  
QY 4321 AACATACTGATTAAGCTCCAGCAGGAAATGGCTGAACCTAGAACCTGTGTGAACAGC 4380  
Db 4321 AACATACTGATTAAGCTCCAGCAGGAAATGGCTGAACCTAGAACCTGTGTGAACAGC 4380  
QY 4381 ATGGGAGCCAGCCTTCTTAACAGCTACCTTCATCATTAAGTACTCTTCCCTTGAAG 4440  
Db 4381 ATGGGAGCCAGCCTTCTTAACAGCTACCTTCATCATTAAGTACTCTTCCCTTGAAG 4440  
QY 4441 ACCGCGAATTCAGAACAAAGCAGATCAGAAAGAGATTAACCTTCAACAGAAAGTA 4500  
Db 4441 ACCGCGAATTCAGAACAAAGCAGATCAGAAAGAGATTAACCTTCAACAGAAAGTA 4500  
QY 4501 GTGAATACCTTATTAAGCAGAAATCCAGAGGCTTCTGTGACAAAGTTTGAAGTGTCTG 4560  
Db 4501 GTGAATACCTTATTAAGCAGAAATCCAGAGGCTTCTGTGACAAAGTTTGAAGTGTCTG 4560  
QY 4561 CAGATAGTCTTACAGTAAATTAAGAACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
Db 4561 CAGATAGTCTTACAGTAAATTAAGAACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
QY 4621 GCCCATATTAGATGATGAGGTGATACATGCAATGTGCTCGGAGAGCTTCAGAAATGAA 4680  
Db 4621 GCCCATATTAGATGATGAGGTGATACATGCAATGTGCTCGGAGAGCTTCAGAAATGAA 4680  
QY 4681 ACTACCATCTCAAGAGAGCTCATTAAGTTGTGTAGTGAAGAGACCAACAGCTGGAAG 4740  
Db 4681 ACTACCATCTCAAGAGAGAGCTCATTAAGTTGTGTAGTGAAGAGACCAACAGCTGGAAG 4740  
QY 4741 AGTGTGGCCACAGATTTGACGAAACATCTTACTTGGCCAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTGTGGCCACAGATTTGACGAAACATCTTACTTGGCCAGGCAAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACTGGAATCTGGAATCAGCCTCTCTGATGAGACCTGAATCTGATCTCTG 4860  
Db 4801 CCCCTTACTGGAATCTGGAATCAGCCTCTCTGATGAGACCTGAATCTGATCTCTG 4860

Db 4801 CCCCTTACTGGAATCTGGAATCAGCCTCTCTGATGAGACCTGAATCTGATCTCTG 4860  
QY 4861 AAGACAGAGCCCCAGAGCTCAGCTGTGTGGCAACATACCATCTTCAACCTCTCATTTGA 4920  
Db 4861 AAGACAGAGCCCCAGAGCTCAGCTGTGTGGCAACATACCATCTTCAACCTCTCATTTGA 4920  
QY 4921 AAGTTCCTCAATTTGAAGTTGACAGATCTGCCAGAGTCCAGCTGTCTCATCTACTG 4980  
Db 4921 AAGTTCCTCAATTTGAAGTTGACAGATCTGCCAGAGTCCAGCTGTCTCATCTACTG 4980  
QY 4981 ATACTGCTGGGTATTAAGCATGGAAGAGTGTGACAGAGGAGAGACCAAGATTTGACAG 5040  
Db 4981 ATACTGCTGGGTATTAAGCATGGAAGAGTGTGACAGAGGAGAGACCAAGATTTGACAG 5040  
QY 5041 CTTTCACAGAAAGGGTCAACAAAGAAATGTCCATGTTGTGTGTGCTGAGTCCAGAGAG 5100  
Db 5041 CTTTCACAGAAAGGGTCAACAAAGAAATGTCCATGTTGTGTGTGCTGAGTCCAGAGAG 5100  
QY 5101 AATTTATGCTGTGTACAGATTTGCCAGAAACACACATCATCTTAACTAATCTAATTA 5160  
Db 5101 AATTTATGCTGTGTGTACAGATTTGCCAGAAACACACATCATCTTAACTAATCTAATTA 5160  
QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGAGTTGTGTGGAAGAGGACAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGAGTTGTGTGGAAGAGGACAC 5220  
QY 5221 TGAATATATTTCTAGAAATTCGCGAGAGAAATGGTAGTAACTATTTCTGCTGAGACC 5280  
Db 5221 TGAATATATTTCTAGAAATTCGCGAGAGAAATGGTAGTAACTATTTCTGCTGAGACC 5280  
QY 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTGG 5340  
Db 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTGG 5340  
QY 5341 TCATGGAAGAAACCAAGAGTCCAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 5400  
Db 5341 TCATGGAAGAAACCAAGAGTCCAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 5400  
QY 5401 TCAAGGGGCTAGAAATCTGTGATGAGGCTTCAACCAATGCCAGAGATCACTGAG 5460  
Db 5401 TCAAGGGGCTAGAAATCTGTGATGAGGCTTCAACCAATGCCAGAGATCACTGAG 5460  
QY 5461 AATGATGATGACAGCTGTGTGTCTGTGTGTGTGAAGAGCTTTATCATTCACCTTG 5520  
Db 5461 AATGATGATGACAGCTGTGTGTCTGTGTGTGTGTGAAGAGCTTTATCATTCACCTTG 5520  
QY 5521 GCACAGGTGTCACCCCAATGTGTGTGTGTGAGCAGATGCTGAGAGAGAGAGAGAGT 5580  
Db 5521 GCACAGGTGTCACCCCAATGTGTGTGTGTGTGAGCAGATGCTGAGAGAGAGAGAGT 5580  
QY 5581 TCCATGCAATTTGGGAGATGTGTGAGCAGCTGTGTGTGTGAGCAGAGTGGGTGTGAGCA 5640  
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGCAGCTGTGTGTGTGAGCAGAGTGGGTGTGAGCA 5640  
QY 5641 GTGTAGCAGCTTACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700  
Db 5641 GTGTAGCAGCTTACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700  
QY 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 6  
LOCUS 181034  
DEFINITION Sequence 1 from patent US 5710001.  
ACCESSION 181034  
NID 93209324  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.



REFERENCE 1 (bases 1 to 5914)  
 AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,  
 Harsman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.  
 and Futreal,P.Andrew.  
 TITLE 17q-linked breast and ovarian cancer susceptibility gene  
 JOURNAL Patent: US 5710001-A 1 20-JAN-1998:  
 FEATURES Location/Qualifiers  
 source 1..5914  
 /organism="unknown"  
 BASE COUNT 2006 a 1156 c 1316 g 1436 t  
 ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5914;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 AGCTCGCTGAGACTCTCTGAGACCCCGACAGCGCTGTGGGTTCTCGATTAAGTGGGC 60
DB 1 AGCTCGCTGAGACTCTCTGAGACCCCGACAGCGCTGTGGGTTCTCGATTAAGTGGGC 60
OY 61 CCTGCGCTCAGAGGCGCTTCAACCTCTGCTGTGGTAAAGTTCAATGGAGAGAA 120
DB 61 CCTGCGCTCAGAGGCGCTTCAACCTCTGCTGTGGTAAAGTTCAATGGAGAGAA 120
OY 121 TGCATTTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCATTATGCTATGCAAAA 180
DB 121 TGCATTTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCATTATGCTATGCAAAA 180
OY 181 TCTTAGAGTCCCATGCTGTGTGAGTTGATCAGGAACCTGTCCCAAGAGTGTACC 240
DB 181 TCTTAGAGTCCCATGCTGTGTGAGTTGATCAGGAACCTGTCCCAAGAGTGTACC 240
OY 241 ACATATTTTTCACAAATTTTGGATGCTGAACCTTCAACACAGAGAAAGGCGTTACAGT 300
DB 241 ACATATTTTTCACAAATTTTGGATGCTGAACCTTCAACACAGAGAAAGGCGTTACAGT 300
OY 301 GTCTTTATATGAAGATGATATTAACCAAGAGAGCTTCAAGAAAGTACGAGATTAGTC 360
DB 301 GTCTTTATATGAAGATGATATTAACCAAGAGAGAGCTTCAAGAAAGTACGAGATTAGTC 360
OY 361 AACTTGTGAAGAGCTATTTGAAATTCATTTTGTCTTTCAGCTTGACAGAGTTGGAGT 420
DB 361 AACTTGTGAAGAGCTATTTGAAATTCATTTTGTCTTTCAGCTTGACAGAGTTGGAGT 420
OY 421 ATGCAAAACAGCTATTAATTTTGCAGAAAGAAATTAACCTCTCTGAACATCTAAAGATG 480
DB 421 ATGCAAAACAGCTATTAATTTTGCAGAAAGAAATTAACCTCTCTGAACATCTAAAGATG 480
OY 481 AAGTTTCTATATCCCAAGATGAGGCTACAGAAACCGTGCAGAAAGAGCTTACAGAGTG 540
DB 481 AAGTTTCTATATCCCAAGATGAGGCTACAGAAACCGTGCAGAAAGAGCTTACAGAGTG 540
OY 541 AACCCGAAATCCTTCTCTCAGAGAAACAGTCTCACTGTCCCACTCTTAACCTTGGAA 600
DB 541 AACCCGAAATCCTTCTCTCAGAGAAACAGTCTCACTGTCCCACTCTTAACCTTGGAA 600
OY 601 CTGTGAGAACTCTGAGAGCAAGAGCGAGATACAACTCAAAAGACGCTGTCTACATTG 660
DB 601 CTGTGAGAACTCTGAGAGCAAGAGCGAGATACAACTCAAAAGACGCTGTCTACATTG 660
OY 661 AATGGATCTGATTTCTTCTGAGATACCGTTAATTAAGCAACTTATGAGAGTGGAG 720
DB 661 AATGGATCTGATTTCTTCTGAGATACCGTTAATTAAGCAACTTATGAGAGTGGAG 720
OY 721 ATCAAGAAATGTACAATACCCCTCAGAGAACAGGAGTGAATGATGTTGATTTCTG 780
DB 721 ATCAAGAAATGTACAATACCCCTCAGAGAACAGGAGTGAATGATGATGTTGATTTCTG 780
OY 781 CAAAAAAGGCTGTTGTGAATTTTCTGAGAGAGATGTAAACAAATACGAAATCATCAAC 840
DB 781 CAAAAAAGGCTGTTGTGAATTTTCTGAGAGAGATGTAAACAAATACGAAATCATCAAC 840

```

```

OY 841 CCAATTAATGATTTTAACACCACTGAGAGAGCTGACGCTGAGAGCATCCGAAAGT 900
DB 841 CCAATTAATGATTTTAACACCACTGAGAGAGCTGACGCTGAGAGCATCCGAAAGT 900
OY 901 ATCAGGAGTGTCTGTTCAAACTGCAATGAGAGCATGTGACACAAATATCATGCCA 960
DB 901 ATCAGGAGTGTCTGTTCAAACTGCAATGAGAGCATGTGACACAAATATCATGCCA 960
OY 961 GCTCATATACAGCATGAGAGAGAGAGTTTATTAATTAATTAAGACAGATGATGAAA 1020
DB 961 GCTCATATACAGCATGAGAGAGAGAGTTTATTAATTAATTAAGACAGATGATGAAA 1020
OY 1021 AGGCTGAATCTGTATTAATAAGCAAGAGCGCTTGTAGAGAGAGCAACATTAAGAT 1080
DB 1021 AGGCTGAATCTGTATTAATAAGCAAGAGCGCTTGTAGAGAGAGCAACATTAAGAT 1080
OY 1081 GGGCTGAGAGTAAAGAAACATGTAATGATGAGGAGATCCACAGAGAGAGAGAGTATG 1140
DB 1081 GGGCTGAGAGTAAAGAAACATGTAATGATGAGGAGATCCACAGAGAGAGAGTATG 1140
OY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAAGAGAAACAGTCCATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAAGAGAAACAGTCCATGCT 1200
OY 1201 CAGAGAAATCCTAAGAGATCTGAAGATGTTCTTGATTAACACTTAATACGATTCAGA 1260
DB 1201 CAGAGAAATCCTAAGAGATCTGAAGATGTTCTTGATTAACACTTAATACGATTCAGA 1260
OY 1261 AAGTTAATGAGTGTGTTTTCAGAGAGATGATGATGTTAGTTTGTATGACTACATGATG 1320
DB 1261 AAGTTAATGAGTGTGTTTTCAGAGAGATGATGATGTTAGTTTGTATGACTACATGATG 1320
OY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATGACGTTCTAAATGAGATGATG 1380
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATGACGTTCTAAATGAGATGATG 1380
OY 1381 AATTTCTGTTCTCTGAGAGAAATAGACTTACTGAGAGAGTATGAGAGGCTTTAA 1440
DB 1381 AATTTCTGTTCTCTGAGAGAAATAGACTTACTGAGAGAGTATGAGAGGCTTTAA 1440
OY 1441 TATGTAAGTGAAGAGTCTCACTCCAAATCACTAAGAGATATATGTAAGACAAATAT 1500
DB 1441 TATGTAAGTGAAGAGTCTCACTCCAAATCACTAAGAGATATATGTAAGACAAATAT 1500
OY 1501 TTGGAGAAACCTATCGGAGAGAGAGAGCTCCCAACTTAAGCCATGTAATCGAAAAATC 1560
DB 1501 TTGGAGAAACCTATCGGAGAGAGAGAGCTCCCAACTTAAGCCATGTAATCGAAAAATC 1560
OY 1561 TAATTAATGAGAGATTTGTTACTGAGAGCAGATTAATTAAGAGAGCTCCCTCACAAATA 1620
DB 1561 TAATTAATGAGAGATTTGTTACTGAGAGCAGATTAATTAAGAGAGCTCCCTCACAAATA 1620
OY 1621 AATTAAGAGTAAAGAGAGAGCTATCAGAGCGCTTATCTGAGATTTTATCAAGAAAG 1680
DB 1621 AATTAAGAGTAAAGAGAGAGCTATCAGAGCGCTTATCTGAGATTTTATCAAGAAAG 1680
OY 1681 CAGATTTGCGAGTTCAAAAGAGCTCTGAATGATTAATCAAGAGAGCTTAAACCAAGAG 1740
DB 1681 CAGATTTGCGAGTTCAAAAGAGCTCTGAATGATTAATCAAGAGAGCTTAAACCAAGAG 1740
OY 1741 AGAATGATCAAGTGAATTAATTAATGATGAGTATGAGATTAATAAGAGAGGAT 1800
DB 1741 AGAATGATCAAGTGAATTAATTAATGATGAGTATGAGATTAATAAGAGAGGAT 1800
OY 1801 CTATTCGAATGAGAGAAATCTTAACCAATAGAAATCACTCGAGAAAGATCTGTTTCA 1860
DB 1801 CTATTCGAATGAGAGAAATCTTAACCAATAGAAATCACTCGAGAAAGATCTGTTTCA 1860
OY 1861 AAACGAAAGCTGAACCTATTAAGAGAGAGATTAAGCAATATGGAATCGAATTAATATCC 1920
DB 1861 AAACGAAAGCTGAACCTATTAAGAGAGAGATTAAGCAATATGGAATCGAATTAATATCC 1920
OY 1921 ACAATTCAAAAAGCACTAAAAAGAAATAGGCTGAGAGAGAGTCTTCTACAGGCAATATTC 1980

```







GenBank Accession Number U15595"  
/db\_xref="taxon:9606"  
/chromosome="17"  
/map="17q21; spans D17S855"  
1..119  
1..100  
/number=1  
101..199  
/number=2  
120..5711  
/gene="BRCA1"  
120..5711  
/gene="BRCA1"  
/note="Influences susceptibility to breast and ovarian cancer"  
/codon\_start=1  
/db\_xref="PID:9555932"  
/translation="MDLSALRVEVQVYINAMOKILBCEPICLELIKRPVSKCDHIPC  
KFCMLKLLNOKGSPGOCPLKNDITKRSIQSTSPFSQVYELLKILICAFOLDPTCLEVA  
NSYMPAKKNSPPLKDEVSITQSGTRNKRKLQSEPEPSELQETSLQSVQSLNIG  
TVRLTRKQRIQPKTSVYIELGSDSSSDYVKNKATYCSVGDELQITPQTRDEL  
DSAKAACFESSEITVTEHNPNSNDLITERKPAERHPEKYOGSSVSNLHVPCT  
NTHASSIQHENSILLTKDRMNVKAEFCNKSQGLARSOHNMAGSKETCNDRRP  
STERKVDLADPLCEKRNKOKLPCSENPRTDTEPMITLNSIQKVENMERSDEL  
LGSDSHDGESENAKAVADVLYNDEVSGSEKIDILADPHHALICKSEVHSK  
SVESNIEDKIRGKTKRKASLPNLSHTENTITGAFTEPOTIOERPLINKLRKRP  
TSGLHPDEFIKADLAVOKTEPMINOGTNOEONGOVNITNSGHENKTKDSIQNK  
NPNDIESLEKSAKTAEPISSEISINNELELNHNSKAPKKNLRKRSRRIHALE  
LVYSRNLSPNCTELQIDSCSSSEIKKKKNOMVRSRNLQMEKEPATGAKKN  
KPNQTSKRHDSDTEPELKLINAPGSPFKSNTSELKEFVPSLPREKEKELTVY  
SNMAEDPKDMLSGEVLQTPERSVSSSISVPTGDTGQDSISLIEVSTGKKTDP  
NKCYSQCAEPENPGLIHGCKDNRNDEGCKRYLGHVNSHRETSIEMSELDAGT  
LQNTFKVSKRQSFAPSPNGAEECAFEASHSLKQSPKVFCEQKENGKME  
SNIPVQTVNTAGFPVVGQDKPDNAKCSIKGSRFCLSSQFNGETGLITPNKKG  
LQMPYRIPPLPIKSEVTKCKKNLLENEEESMSPEREMENIPSTVSTSRNN  
IRENVFEASSNINEGSSNINEGSSNINEGSSNINEGSSNINEGSSNINEGSSN  
LOPEVYKOSLPGSNCKHPEIKKQYEVEYVOTVNTDFSYLSDNLQPMGSHASQVC  
SETPDLLDDEIKEDISFANDIKESANVSKSVQKGLSRSPPTHTHLAGCYR  
GAKLSESEENLSEDELPFOHLFGKVNILISQSTRHSTVATECLSKTEENLIS  
LKNLINDCSNOVILAKAQEHNLSEETCSALPSQCSSELEDITANTINDPTELLS  
SKOMRHQSEQVGLSDKELVSDDEKGTGLEENNOLEQVSDMSHGAASCESETVY  
SEDCSGSSOSDILITTOORDIMONHLIKLOEAMLEAVLEOHGOSPSNSPSTISNS  
SALDELNPNETSEKAVLITQSSSEYPISONPGLSADKFEVADSSTSKNKPCVE  
RSFSPKPSLDDRTYHNSGSGSLQNRNTPSEBELIKVADVEBQLESQPDULTYST  
LPRODLEGPYLEGISLFSDDPSDSEDAEPSARAGNIPSSISLAKVQLVAAS  
AQSPAATHTDTAGYNAMEESVSREKPELITSTERYKRMGMVSGLPPEFMYVAF  
ARKHILITLNLITEETHYVAKTDAEFVCEERTLKYFLGAGKVVVSYFVWTQIKER  
KMLNEHPEVGVGADVNGRNHOGPKRARESDORKLFRGLETCCYCPPTNMPDQLEMY  
OLGASVYKELSFSTIGVHPPIYVQPDANTEDNGHAIQMCBAEVYRREVLDSV  
ALYCCQEDLITLIQIPIHSHY"  
200..253  
/gene="BRCA1"  
/number=3  
254..331  
/gene="BRCA1"  
/number=5  
332..420  
/gene="BRCA1"  
/number=6  
421..560  
/gene="BRCA1"  
/number=7  
561..665  
/gene="BRCA1"  
/number=8  
666..712  
/gene="BRCA1"  
/number=9  
713..788  
/gene="BRCA1"  
/number=10  
789..4215  
/gene="BRCA1"

exon	/number=11	4216..4302	/gene="BRCA1"
exon	/number=12	4303..4476	/gene="BRCA1"
exon	/number=13	4477..4603	/gene="BRCA1"
exon	/number=14	4604..4794	/gene="BRCA1"
exon	/number=15	4795..5105	/gene="BRCA1"
exon	/number=16	5106..5193	/gene="BRCA1"
exon	/number=17	5194..5273	/gene="BRCA1"
exon	/number=18	5274..5310	/gene="BRCA1"
exon	/number=19	5311..5396	/gene="BRCA1"
exon	/number=20	5397..5451	/gene="BRCA1"
exon	/number=21	5452..5526	/gene="BRCA1"
exon	/number=22	5527..5586	/gene="BRCA1"
exon	/number=23	5587..5711	/gene="BRCA1"
exon	/number=24		
BASE COUNT	1956 a	1099 c	1274 g
1382 t			
ORIGIN			
Query Match	100.0%;	Score 5709.4;	DB 10; Length 5711;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 5710;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
1	AGCTGCGTGAACACTTCTCGGACCCCGCACCGAGCTGTGGGTTCTCAGATTAAGTGGCC	60	
1	AGCTGCGTGAACACTTCTCGGACCCCGCACCGAGCTGTGGGTTCTCAGATTAAGTGGCC	60	
61	CCTGCGCTCAGAGAGCCCTTCAACCTCTGCTGGGTAAAGTTGGAACAGAAAGAA	120	
61	CCTGCGCTCAGAGAGCCCTTCAACCTCTGCTGGGTAAAGTTGGAACAGAAAGAA	120	
121	TGGAATTAATCTGCTCTCGCGTTGAGAAGTACAAATGTATTATATGCTATGAGAAA	180	
121	TGGAATTAATCTGCTCTCGCGTTGAGAAGTACAAATGTATTATATGCTATGAGAAA	180	
121	TGGAATTAATCTGCTCTCGCGTTGAGAAGTACAAATGTATTATATGCTATGAGAAA	180	
181	TCTTGAAGTGTCCCATCTGTGTGAGAGTATGATCAAGAACCTGTCTCCCAAAAGTGTACC	240	
181	TCTTGAAGTGTCCCATCTGTGTGAGAGTATGATCAAGAACCTGTCTCCCAAAAGTGTACC	240	
241	ACATATTTTGAATTTTGCATGCTGAACCTTCAACCCAGAGAAAGGCGCTCACAGT	300	
241	ACATATTTTGAATTTTGCATGCTGAACCTTCAACCCAGAGAAAGGCGCTCACAGT	300	
301	GTCCTTATGTAGATATGATTAACCAAAAGAGCCTACAAAGAAAGTACGAGATTAGTC	360	
301	GTCCTTATGTAGATATGATTAACCAAAAGAGCCTACAAAGAAAGTACGAGATTAGTC	360	
361	AACCTGTGTAAGACCTATGAAATTCATTGTGCTTTACGCTTGACACAGGTTTGAGT	420	

```
Db 361 AACTGTGGAAGACTATGAAAAATCATTTGTGCTTTACACTTGACACAGTTGGAGT 420
Qy 421 ATGCAACAGCTATTAATTTTSCAAAAAGAAATTAAGTCTCTGTAATCTTAAGATG 480
Db 421 ATGCAACAGCTATTAATTTTSCAAAAAGAAATTAAGTCTCTGTAATCTTAAGATG 480
Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAAGACTTCTACAGATG 540
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAAGACTTCTACAGATG 540
Qy 541 AACCCGAAATTCCTTCTTGAGGAAACCACTCAAGTGTCCAACTCTTAACCTTGAA 600
Db 541 AACCCGAAATTCCTTCTTGAGGAAACCACTCAAGTGTCCAACTCTTAACCTTGAA 600
Qy 601 CTGTGAGACTCTGAGGCAAGACAGCGGATACAACCTCAAAAGAGCTGTCTCATATG 660
Db 601 CTGTGAGACTCTGAGGCAAGACAGCGGATACAACCTCAAAAGAGCTGTCTCATATG 660
Qy 661 AATTTGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATTGCAAGTGGAG 720
Db 661 AATTTGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATTGCAAGTGGAG 720
Qy 721 ATGAGAAATTTGTTCAATATCCCTCAAGGAAACGAGGATGAATCATGTTGATCTG 780
Db 721 ATGAGAAATTTGTTCAATATCCCTCAAGGAAACGAGGATGAATCATGTTGATCTG 780
Qy 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGTAAACAATTAAGTCAATCAAC 840
Db 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGTAAACAATTAAGTCAATCAAC 840
Qy 841 CCAATTAATTAATGATTTGAACACCACTGAAAGCGTGACGTGAGAGCATCCAGAAAGT 900
Db 841 CCAATTAATTAATGATTTGAACACCACTGAAAGCGTGACGTGAGAGCATCCAGAAAGT 900
Qy 901 ATGAGGATCTGCTGTTCAAACTTGATGAGGCACTGAGGCACTGAGCAAACTCATGCA 960
Db 901 ATGAGGATCTGCTGTTCAAACTTGATGAGGCACTGAGGCACTGAGCAAACTCATGCA 960
Qy 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGAATGAGAA 1020
Db 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGAATGAGAA 1020
Qy 1021 AAGCTGAATCTGTAATTAAGCAACAGCTGGCTTACGAAGAGCCACATTAACAGAT 1080
Db 1021 AAGCTGAATCTGTAATTAAGCAACAGCTGGCTTACGAAGAGCCACATTAACAGAT 1080
Qy 1081 GGGCTGGAAGTAAGGAACAATGTAATGAGGAGACTCCAGCAGCAAGAAAAAGTAG 1140
Db 1081 GGGCTGGAAGTAAGGAACAATGTAATGAGGAGACTCCAGCAGCAAGAAAAAGTAG 1140
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGCAGAACTGCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGCAGAACTGCCATGCT 1200
Qy 1201 CAGAGAACTCTAAGATACCTGGAAGATGTTCTTGATTAACCTTAATAGCAGATTCGA 1260
Db 1201 CAGAGAACTCTAAGATACCTGGAAGATGTTCTTGATTAACCTTAATAGCAGATTCGA 1260
Qy 1261 AAGTTAATGAGTGGTTTCCAGAGATGTAAGTGAAGTTCGATGACACATGATG 1320
Db 1261 AAGTTAATGAGTGGTTTCCAGAGATGTAAGTGAAGTTCGATGACACATGATG 1320
Qy 1321 GGGAGTCTGAATCAAAATGCAAAAGTAGCTGATTAATGAGAGTTCCTAATAGGTAGTG 1380
Db 1321 GGGAGTCTGAATCAAAATGCAAAAGTAGCTGATTAATGAGAGTTCCTAATAGGTAGTG 1380
Qy 1381 AATATTTCTGTTCTTCAGAGAAAAATAGACTTACGGCAGTGAATCTCATAGGCTTTAA 1440
Db 1381 AATATTTCTGTTCTTCAGAGAAAAATAGACTTACGGCAGTGAATCTCATAGGCTTTAA 1440
Qy 1441 TATGTAAAAGTGAAGAGTCACTCCAAATCAGTAGAGATTAATTGAAGCAAAATAT 1500
Db 1441 TATGTAAAAGTGAAGAGTCACTCCAAATCAGTAGAGATTAATTGAAGCAAAATAT 1500
Qy 1501 TTGGGAAACCTATCGGAGAGAGCAAGCCTCCCAACTTAAGCCTGAATGAAATATC 1560
Db 1501 TTGGGAAACCTATCGGAGAGAGCAAGCCTCCCAACTTAAGCCTGAATGAAATATC 1560
Qy 1561 TAATTTATGAGACATTTGTTACTAGGCAACAGATTAATACAGAGCTCCCTACAAATA 1620
Db 1561 TAATTTATGAGACATTTGTTACTAGGCAACAGATTAATACAGAGCTCCCTACAAATA 1620
Qy 1621 AATTAAGCGTAAAAGAGAGCTCATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680
Db 1621 AATTAAGCGTAAAAGAGAGAGCTCATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGGAATCAACAAAGGAGC 1740
Db 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGGAATCAACAAAGGAGC 1740
Qy 1741 AGAATGGTCAAGTATGATTAATTTACTAATATGAGTGCATGAGAAATAACAAAGTGAT 1800
Db 1741 AGAATGGTCAAGTATGATTAATTTACTAATATGAGTGCATGAGAAATAACAAAGTGAT 1800
Qy 1801 CTATTCAAGATGAGAAAAATCTTAACCAATAGATCACTGCAAAAAAGATGCTTTCA 1860
Db 1801 CTATTCAAGATGAGAAAAATCTTAACCAATAGATCACTGCAAAAAAGATGCTTTCA 1860
Qy 1861 AAGCAAGGCTGAACCTTAAGCAGCAGTAAAGCAATATGAACTGAAATTAATATCC 1920
Db 1861 AAGCAAGGCTGAACCTTAAGCAGCAGTAAAGCAATATGAACTGAAATTAATATCC 1920
Qy 1921 ACAATTTAAAAGCACTTAAGAAATAGGCTGAGGAGAAAGTCTTACAGGCAATATTC 1980
Db 1921 ACAATTTAAAAGCACTTAAGAAATAGGCTGAGGAGAAAGTCTTACAGGCAATATTC 1980
Qy 1981 ATGCGCTTGAAGTATGATGATGAGAAATTAAGCCACCTAATTTACTGATTAATCA 2040
Db 1981 ATGCGCTTGAAGTATGATGATGAGAAATTAAGCCACCTAATTTACTGATTAATCA 2040
Qy 2041 TTGATAGTGTCTTACAGTGAAGAGATTAAGAAAAAGTAAACAACAAATGCCAGTCA 2100
Db 2041 TTGATAGTGTCTTACAGTGAAGAGATTAAGAAAAAGTAAACAACAAATGCCAGTCA 2100
Qy 2101 GGCACACAGAAACCTTAACATCATGGAAGGTAAGAACTGCACTGAGCCAGAGAGA 2160
Db 2101 GGCACACAGAAACCTTAACATCATGGAAGGTAAGAACTGCACTGAGCCAGAGAGA 2160
Qy 2161 GTAACAAGCCAAATGAACAGACATGAAAGAGATACAGAGCTACTTCCAGAGCTGA 2220
Db 2161 GTAACAAGCCAAATGAACAGACATGAAAGAGATACAGAGCTACTTCCAGAGCTGA 2220
Qy 2221 AGTTAACAAATGCACCTGTTCTTTACTAAGTGTCAATACACAGTGAATGAAGAT 2280
Db 2221 AGTTAACAAATGCACCTGTTCTTTACTAAGTGTCAATACACAGTGAATGAAGAT 2280
Qy 2281 TTGTCAATCTTACGCTTCCAGAGAGAAAAAGAAAGAACTAGAAAGTAAAGTGT 2340
Db 2281 TTGTCAATCTTACGCTTCCAGAGAGAAAAAGAAAGAACTAGAAAGTAAAGTGT 2340
Qy 2341 CTAAATATGCTGAAGAGCCCAAGATCTCATGTTAAGTGAAGAGGTTTTCGAAACAG 2400
Db 2341 CTAAATATGCTGAAGAGCCCAAGATCTCATGTTAAGTGAAGAGGTTTTCGAAACAG 2400
Qy 2401 AAGATCTGTAGAGAGTGAAGATTTTCAATTTGTTACTGCTGACTGATTAATGCACTCAG 2460
Db 2401 AAGATCTGTAGAGAGTGAAGATTTTCAATTTGTTACTGCTGACTGATTAATGCACTCAG 2460
Qy 2461 AAGATCTGTGTTACTGAGAGTGTAGCACTCTAGGAGGCAAAACAGAACTTAAT 2520
Db 2461 AAGATCTGTGTTACTGAGAGTGTAGCACTCTAGGAGGCAAAACAGAACTTAAT 2520
Qy 2521 GTGTGAGTCAAGTGCAGCACTTGAAGAAACCCCAAGGAGCTAATTTATGTTTCCAAAG 2580
Db 2521 GTGTGAGTCAAGTGCAGCACTTGAAGAAACCCCAAGGAGCTAATTTATGTTTCCAAAG 2580
```

QY	2581	ATATAGAAATGACACGAGAGCGCTTTAAATGATCCATTTGGGACATGAAGTTAACCAAGCTC	2640
Db	2581	ATAATAGAAAGACACGAGAGCGCTTTAAATGATCCATTTGGGACATGAAGTTAACCAAGCTC	2640
QY	2641	GGGAAACAGCATGTGAATGGAAGAAAGTGAACCTTATCTCAGTATTGTGCGAATACAT	2700
Db	2641	GGGAAACAGCATGTGAATGGAAGAAAGTGAACCTTATCTCAGTATTGTGCGAATACAT	2700
QY	2701	TCGAGTTTCAAGCGCCAGTCAATTTGCTGTGTTTTCAATCCAGGAAATGCGAAGAGG	2760
Db	2701	TCGAGTTTCAAGCGCCAGTCAATTTGCTGTGTTTTCAATCCAGGAAATGCGAAGAGG	2760
QY	2821	TTGATGTGAACAAAGAGAAATATCAAGAAAGATGACTAATATCAAGCCTGTAC	2880
Db	2821	TTGATGTGAACAAAGAGAAATATCAAGAAAGATGACTAATATCAAGCCTGTAC	2880
QY	2881	AGACAGTTAATATCACGCGAGCGCTTTCCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACGCGAGCGCTTTCCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA	2940
QY	2941	ATGCCAATGTAGATCAAAAGAGAGCGCTAGTGGTTTGCTATCATCTCAGTCCAGAGACA	3000
Db	2941	ATGCCAATGTAGATCAAAAGAGAGCGCTAGTGGTTTGCTATCATCTCAGTCCAGAGACA	3000
QY	3001	ACGAACTGCATCTATTCCTCAATTAACATGAGACTTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAACTGCATCTATTCCTCAATTAACATGAGACTTTTACAAAACCCATATCGTATAC	3060
QY	3061	CACACCTTTTCCCATCAATCAATCTGTTGTTTAAACCTAAATGTAGAAAAATCTCGTAGAGG	3120
Db	3061	CACACCTTTTCCCATCAATCAATCTGTTGTTTAAACCTAAATGTAGAAAAATCTCGTAGAGG	3120
QY	3121	AAAACTTGGAGAACATTTCAATGTCACTGTAAGAGAAATGGGAAATGAGAACATTTCCA	3180
Db	3121	AAAACTTGGAGAACATTTCAATGTCACTGTAAGAGAAATGGGAAATGAGAACATTTCCA	3180
QY	3181	GTACAGTGAGACACAATTAGGCCGTTATTAACATTTAGAAAAATGTTTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTGAGACACAATTAGGCCGTTATTAACATTTAGAAAAATGTTTTTAAAGAGCCAGCT	3240
QY	3241	CAAGCAATATTAATGAAGTAGTGTCCAGTACTATGAATGGGCTCCAGTATTATTAAGAA	3300
Db	3241	CAAGCAATATTAATGAAGTAGTGTCCAGTACTATGAATGGGCTCCAGTATTATTAAGAA	3300
QY	3301	TAGGTTCCAGTGATGAAGAACATTCAGACAGACTAGTGAAGAAACAGAGGCCCAAAATTGA	3360
Db	3301	TAGGTTCCAGTGATGAAGAACATTCAGACAGACTAGTGAAGAAACAGAGGCCCAAAATTGA	3360
QY	3361	ATGCTATGCTTAGGTTTGGGGTTTTGCAACCTGAGGCTATTAACAAAGTCTCTCTGGAA	3420
Db	3361	ATGCTATGCTTAGGTTTGGGGTTTTGCAACCTGAGGCTATTAACAAAGTCTCTCTGGAA	3420
QY	3421	GTAATTGTAAAGCATCTGAAATAAAAAGCAGAAATNTGAAGAGTAGTTGACAGCTGTTA	3480
Db	3421	GTAATTGTAAAGCATCTGAAATAAAAAGCAGAAATNTGAAGAGTAGTTGACAGCTGTTA	3480
QY	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAACACAGCCTATGGAGTAGTC	3540
Db	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAACACAGCCTATGGAGTAGTC	3540
QY	3541	ATGCATCTCAGGTTGTGTTGAGACACGTAATGACTGTTTAATATGTGTAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTGTGTTGAGACACGTAATGACTGTTTAATATGTGTAATTAAGG	3600
QY	3601	AAGATACTAGTTTGTCTGAAATGACATTTAGGAAAGTTCTGCTGTTTTAGCAAAACGG	3660
Db	3601	AAGATACTAGTTTGTCTGAAATGACATTTAGGAAAGTTCTGCTGTTTTAGCAAAACGG	3660

QY	3661	TCGAGAAAGGAGACCTTAGCGNAGAGTCCTTAGCCCTTTCACCCATACATATTGGCTCAG	3720
QY	3661	TCGAGAAAGGAGACCTTAGCGNAGAGTCCTTAGCCCTTTCACCCATACATATTGGCTCAG	3720
Db	3661	TCGAGAAAGGAGACCTTAGCGAGAGTCCTTAGCCCTTTCACCCATACATATTGGCTCAG	3720
QY	3721	GTTACCGAAGGGGGCCAGAAATTAGAGTCCTCAGAAAGAACTTATCTAGTGGATG	3780
Db	3721	GTTACCGAAGGGGGCCAGAAATTAGAGTCCTCAGAAAGAACTTATCTAGTGGATG	3780
QY	3781	AAGAGCTCCCTGCTCCAAACACTTGTATTGTAAGTAAACAATATACCTTCAGT	3840
Db	3781	AAGAGCTCCCTGCTCCAAACACTTGTATTGTAAGTAAACAATATACCTTCAGT	3840
QY	3841	CTACTAGGCATAGCAACCGCTTGTCACGAGTCGTCTTAAGAACACAGAGGAATTTAT	3900
Db	3841	CTACTAGGCATAGCAACCGCTTGTCACGAGTCGTCTTAAGAACACAGAGGAATTTAT	3900
QY	3901	TATCATTTAATAAATAGCTTTAAATGACATCGCTAACCGATATATTGGCAAGGCATCTC	3960
Db	3901	TATCATTTAATAAATAGCTTTAAATGACATCGCTAACCGATATATTGGCAAGGCATCTC	3960
QY	3961	AGGAACATCACCTTAGTAGAGAAACAATAATGTTCTGCTAGCTGTGTTTCTTCACAGTCA	4020
Db	3961	AGGAACATCACCTTAGTAGAGAAACAATAATGTTCTGCTAGCTGTGTTTCTTCACAGTCA	4020
QY	4021	GTTGAATTGGGAAGACTGTGACTGTCAAATACAAACACCCAGATCCTTTCGATTGGTCTT	4080
Db	4021	GTTGAATTGGGAAGACTGTGACTGTCAAATACAAACACCCAGATCCTTTCGATTGGTCTT	4080
QY	4081	CCAAACAAATAGGCATACGTCGTGAAACCCAGGAGATTGCTGAGTACAAAGAAATTGG	4140
Db	4081	CCAAACAAATAGGCATACGTCGTGAAACCCAGGAGATTGCTGAGTACAAAGAAATTGG	4140
QY	4141	TTTCGATGATGAAGAAAGAGAACGGGCTTGGAAATAAATAATCAAGAGCAAAACA	4200
Db	4141	TTTCGATGATGAAGAAAGAGAACGGGCTTGGAAATAAATAATCAAGAGCAAAACA	4200
QY	4201	TGGATTCAAACCTAGTGTAGACACACATCTGGGTGTGAGAGTAAACACGCTCTGTAAG	4260
Db	4201	TGGATTCAAACCTAGTGTAGAGACACATCTGGGTGTGAGAGTAAACACGCTCTGTAAG	4260
QY	4261	ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAACCACTCAGCAGAGGGATACCAATGC	4320
Db	4261	ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAACCACTCAGCAGAGGGATACCAATGC	4320
QY	4321	AACATTAACCTTAAACGCTCAGCAGAGAAATGGCTAATTAAGACGCTGTTAGAACACG	4380
Db	4321	AACATTAACCTTAAACGCTCAGCAGAGAAATGGCTAATTAAGACGCTGTTAGAACACG	4380
QY	4381	ATGGAGGCAAGCCTTCTAACAGCTTACCCTTCATCAATTAAGTACTCTCTGCCTTGAAG	4440
Db	4381	ATGGAGGCAAGCCTTCTAACAGCTTACCCTTCATCAATTAAGTACTCTCTGCCTTGAAG	4440
QY	4441	ACCTGCGAAATCCGAAACAAAGCAGATCAAAAAAACAGTATTAACTTACAGAAAATA	4500
Db	4441	ACCTGCGAAATCCGAAACAAAGCAGATCAAAAAAACAGTATTAACTTACAGAAAATA	4500
QY	4501	GTGAATTAACCTTAATAGGCAGAAATCCAGAAAGGCTTCTCTCTACAGTTTGAAGTGTG	4560
Db	4501	GTGAATTAACCTTAATAGGCAGAAATCCAGAAAGGCTTCTCTCTACAGTTTGAAGTGTG	4560
QY	4561	CAGATAGTTTCAACAGTAAATAAAGAACAGAGATGGAAAGTCATCCCTTTTAAT	4620
Db	4561	CAGATAGTTTCAACAGTAAATAAAGAACAGAGATGGAAAGTCATCCCTTTTAAT	4620
QY	4621	GCCCATCTTTAGATAGTGGTGTACATGCACAGTTGCTCTGGAGTCTTCAGATATAGA	4680
Db	4621	GCCCATCTTTAGATAGTGGTGTACATGCACAGTTGCTCTGGAGTCTTCAGATATAGA	4680
QY	4681	ACTACCATCTCAAGAGAGCTCATTAAGGTGTTGTAATGAGAGGCAACAGCTGGAG	4740
Db	4681	ACTACCATCTCAAGAGAGCTCATTAAGGTGTTGTAATGAGAGGCAACAGCTGGAG	4740
QY	4741	AGTCTGGGCGCACAGATTTCAGGAAACATCTTACTTGCACAGGCAAGATCTAGAGGAA	4800

Db	4741	AGTCTGGGCCACAGATTGTTCGGAATCATTTACTTGCCCAAGCAGAATCTTAGCGAA	4800
Oy	4801	CCCCTTAACCTGGAAATCTGGAAATCACGCTCTTCTGTATGACCCTGAATCTGATCCTTGTG	4860
Db	4801	CCCCTTAACCTGGAAATCTGGAAATCACGCTCTTCTGTATGACCCTGAATCTGATCCTTGTG	4860
Oy	4861	AAGCAGAGCCCCAGAGATCAGCTGCTGTGGCACTATCACATCTTCAACCTCTGCATTGA	4920
Db	4861	AAGCAGAGCCCCAGAGATCAGCTGCTGTGGCACTATCACATCTTCAACCTCTGCATTGA	4920
Oy	4921	AAGTCCCACAATTGAAAGTTGCAGAAATCTGCCAGATCCAGCTGCTGCTATCACTACTG	4980
Db	4921	AAGTCCCACAATTGAAAGTTGCAGAAATCTGCCAGATCCAGCTGCTGCTATCACTACTG	4980
Oy	4981	ATPCTCTGGGTATTAATGCAATGGAAGAAGTGAACAGGAGAAACCGAATATTCAG	5040
Db	4981	ATPCTCTGGGTATTAATGCAATGGAAGAAGTGAACAGGAGAAACCGAATATTCAG	5040
Oy	5041	CCTTCAACAGAAAGGCTCACAAAAGAATGTCATGCTGTGTCTGCGCTGACCCACAG	5100
Db	5041	CCTTCAACAGAAAGGCTCACAAAAGAATGTCATGCTGTGTCTGCGCTGACCCACAG	5100
Oy	5101	AATTTATGCGCGGTGACAACTGTTGCCGAAAAACCAACATCACTTTAACTAATTA	5160
Db	5101	AATTTATGCGCGGTGACAACTGTTGCCGAAAAACCAACATCACTTTAACTAATTA	5160
Oy	5161	CTGAAAGACTACTCATGTGTGTTATGAAAACAGATGCTGAGTTGTGTGTGAACGACAC	5220
Db	5161	CTGAAAGACTACTCATGTGTGTTATGAAAACAGATGCTGAGTTGTGTGTGAACGACAC	5220
Oy	5221	TGAAAATATTTCTAGSAAATTCGCGGAGAAAATGGGAGTAGCTATTCTGTGGGTGACC	5280
Db	5221	TGAAAATATTTCTAGSAAATTCGCGGAGAAAATGGGAGTAGCTATTCTGTGGGTGACC	5280
Oy	5281	AGCTCTTTAAAGAAAATAAATCTGTAATGAGCATGTTTGAAGTCAGAGGAGATGTGG	5340
Db	5281	AGCTCTTTAAAGAAAATAAATCTGTAATGAGCATGTTTGAAGTCAGAGGAGATGTGG	5340
Oy	5341	TCAATGGAAGAAACCAACCAAGTCCAAAAGCAGCAAGAGATCCACAGACAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCAACCAAGTCCAAAAGCAGCAAGAGATCCACAGACAGAAAGATCT	5400
Oy	5401	TGAGGGGGCTAGAAATCTGTGCTATGSGGCCCTTCCACAATGCCCACAGATCACTGG	5460
Db	5401	TGAGGGGGCTAGAAATCTGTGCTATGSGGCCCTTCCACAATGCCCACAGATCACTGG	5460
Oy	5461	AATGATGTGTACAGCTGTGTGTGCTTCTGTGTGTAAGAGAGCTTTCATCTACACCTTG	5520
Db	5461	AATGATGTGTACAGCTGTGTGTGCTTCTGTGTGTAAGAGAGCTTTCATCTACACCTTG	5520
Oy	5521	GCACAGGTGTCACCAATTTGTGTGTGTGACGACAGATGCTGTGACAGAGACATGCT	5580
Db	5521	GCACAGGTGTCACCAATTTGTGTGTGTGACGACAGATGCTGTGACAGAGACATGCT	5580
Oy	5581	TCCATGCAATTTGGCGAGATGTGTGAGAGCACTGTGTGTGACCCAGAGTGGGTITGGACA	5640
Db	5581	TCCATGCAATTTGGCGAGATGTGTGAGAGCACTGTGTGTGACCCAGAGTGGGTITGGACA	5640
Oy	5641	GTTGACACTTACCAAGTGTGAGAGCACTGTGTGACCCAGAGTGGGTITGGACA	5700
Db	5641	GTTGACACTTACCAAGTGTGAGAGCACTGTGTGACCCAGAGTGGGTITGGACA	5700
Oy	5701	GCCACTACTGA	5711
Db	5701	GCCACTACTGA	5711
RESULT	8		
HSU14680	5711 bp	mRNA	PRI 05-AUG-1995
LOCUS	HSU14680		
DEFINITION	Human breast and ovarian cancer susceptibility (BRCA1) mRNA,		
	complete cds.		

ACCESSION	UT14680
NID	9555931
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotes: mitochondrial eukaryotes; Metazoa: Chordata: Vertebrata: Euteheria; Primates; Catarrhini: Homiidae: Homo. 1 (bases 1 to 5711)
AUTHORS	Miki Y., Swensen J., Shattuck-Eidens D., Futreal P.A., Harsman K., Tavligian S., Liu Q., Cochran C., Bennett L.M., Ding W., Bell R., Rosenthal J., Hussey C., Tran T., McClure M., Frye C., Hattier T., Phelps R., Haugen-Strano A., Katcher H., Yakumo K., Gholami Z., Shafer D., Stone S., Bayer S., Wray C., Bogden K., Dayanath P., Ward J., Tonin P., Narod S., Bristow P.K., Norris F.H., Helvering L., Morrison P., Kosteck P., Lai M., Barrett J.C., Lewis C., Neuhansen S., Cannon-Albright L., Goldgar D., Wiseman R., Kamb A. and Skolnick M.H.
TITLE	A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1
JOURNAL	Science 266 (5182), 66-71 (1994)
MEDLINE	95025896
REFERENCE	2 (bases 1 to 5711)
AUTHORS	Skolnick, M.H.
TITLE	Direct Submission
JOURNAL	Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc., and the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City, UT 84108, USA
FEATURES	Location/Qualifiers
SOURCE	1..5711 /organism="Homo sapiens" /note="For sequence of alternatively spliced exon 4, see GenBank Accession Number U15595" /db_xref="taxon:9606" /chromosome="17" /map="17q21; spans D17S855" 1..119 1..100 /number=1 101..199 /number=2 120..5711 /gene="BRCA1" 120..5711 /gene="BRCA1" /note="Influences susceptibility to breast and ovarian cancer" /codon_start=1 /db_xref="PID:9555932" /translation="MDLSLRVREYVNYINAMOKITIEPCILEIKELIPEVSTKCHIFC KFLMLLWKKGPSCPLKNDITKRSIQESTRSQIVLEELIKITICAAQIDLTGLETA NSNENFKKNNSEBHLKDEVSIIQSGMYENRNRKRLQSGSEPNPSLOEISLVOLGSL YATLTETKROIOPKTSYIELGSDSEEDTVAKATGCSVGDELLOITPOGRDEISL DSKAKKAAECSETDVTNTHOHPNSNDLWTEKRAERPEKYOSSVSNLHVEECGT NTHASLHGENSILLTKTRMVERAEFENCKSGKGLAOSHNNRAKSEFCNDNRPT SEETKQIDLADPLCEKKEWKKKLCQSENPRTDTEVPATTLSIQKVENRSDEL LSGDSHDDESSENAKVDYLYLNEVDYSSSEKTDILADPHEALPTKRRKRP SVESNIEDKIFGKTYRKKASLPNLHVENLLIGAVEPQIIORPLTKRRKRP TSGLHEDIEIKRADLVQKTPEMINOGTFOFQNOQVNNITSGHENKTKDSIONEK NNPILEIELESKAEATKAPISISSINMELIINSKRPKRRLRRKSTGHIALE LVSYRLSPNCTELOIDCSSESEIKKKKYOMPYRHSRNLQIMGEGPAGKARKS NKNQESKRSHDDTPELKTINAPGSFTKCSSTELKFFVNNIIPREKEELRYKV SNNADPRDMLSGERYLDTKRSYESSLSILYPTGIDYGQESISLSEYSTLKATPE NNCVSCAFAENPKGLIHGCSKDNKNDTGEFYPLGHEVHNSRETISEEESLADQY LQNTKRSKROSFAPSPNGNAEECAFSAHSGSLKQSPKVTPECEQKEENQCKE SNIKPQVATINATGAPVVGQDKRPVDNAKCSIKGSRPLCSQFGNEGILTPKRG LKQNPVPLPIPKISFYTKKCKNLLNEPEHSGMSPREMGNNIPISVATISRN IRENYEKASSNNINAVGSSINIEGSSNDQALGRRGRCIKNAMLCY LQPEYVKQSPGSSNCKHPETIKQYEBEVQYVNTDPSPLISDNLQPMGSHASQV SETPDLDLDGELIKEDTSAENDIKESSAVEKSVQKQELSPSPFTPHLAAQYR GAKTSLDESSEENLSDEBELPCFQHLFFKVVNNIPQSTRHSVATKCTSKNTENILS LKNSLDCSNQVILAKRASQEHLSSETKCSASLFSQCSCELDLANTDQDPLTGS SKOMKRSQSGVGLDEKELVADDERGEGLEENNOQNSNIGEAASQCESTVS SMDCSGISQSSQNTITTOORPTMOMHLLTIQOMALFAVITRHSQSPNSVDSITSDS



SALEDLRNPBSTSEKAVLTSOKSESEPISONPEGLSADKFEVSADSTSKNKEPGE  
 RSSPBRKPSLIDRMTMHSCSSGLONRNPSPBELIKYDVEQOIEBGPDIETST  
 LPRDLESTPYLESIGLSLSDPESDPESDAPESARVGNIPSSISALKPOLVAES  
 AOSPAATPTDIAGNAMEESVSREKPELTAISTERVNRMSMNVVSGLPDEFMVKR  
 ARKHITLTLNLTETTHVVKMTDAEFVCEKTLKFLGIAGKVVSYFVWOSIKER  
 KMLNDEFEVDVYGNRHOQPKRARESORKIPRGIEICCYGPTMPIDOLEMY  
 OLCCASVYKELSEFTIGTVHPPIVVQPDATNEENGFIATGOMCEAPVYTHENWLDVS  
 ALXOCQELDTILIPHPSHY"

exon /gene="BRCA1"  
 /number=3  
 254..331  
 /gene="BRCA1"  
 /number=5  
 332..420  
 /gene="BRCA1"  
 /number=6  
 421..560  
 /gene="BRCA1"  
 /number=7  
 561..665  
 /gene="BRCA1"  
 /number=8  
 666..712  
 /gene="BRCA1"  
 /number=9  
 713..788  
 /gene="BRCA1"  
 /number=10  
 789..4215  
 /gene="BRCA1"  
 /number=11  
 4216..4302  
 /gene="BRCA1"  
 /number=12  
 4303..4476  
 /gene="BRCA1"  
 /number=13  
 4477..4603  
 /gene="BRCA1"  
 /number=14  
 4604..4794  
 /gene="BRCA1"  
 /number=15  
 4795..5105  
 /gene="BRCA1"  
 /number=16  
 5106..5193  
 /gene="BRCA1"  
 /number=17  
 5194..5273  
 /gene="BRCA1"  
 /number=18  
 5274..5310  
 /gene="BRCA1"  
 /number=19  
 5311..5396  
 /gene="BRCA1"  
 /number=20  
 5397..5451  
 /gene="BRCA1"  
 /number=21  
 5452..5526  
 /gene="BRCA1"  
 /number=22  
 5527..5586  
 /gene="BRCA1"  
 /number=23  
 5587..5711  
 /gene="BRCA1"  
 /number=24  
 5712..5886  
 /gene="BRCA1"  
 /number=25  
 5887..6000  
 /gene="BRCA1"  
 /number=26  
 6001..6115  
 /gene="BRCA1"  
 /number=27  
 6116..6230  
 /gene="BRCA1"  
 /number=28  
 6231..6345  
 /gene="BRCA1"  
 /number=29  
 6346..6460  
 /gene="BRCA1"  
 /number=30  
 6461..6575  
 /gene="BRCA1"  
 /number=31  
 6576..6690  
 /gene="BRCA1"  
 /number=32  
 6691..6805  
 /gene="BRCA1"  
 /number=33  
 6806..6920  
 /gene="BRCA1"  
 /number=34  
 6921..7035  
 /gene="BRCA1"  
 /number=35  
 7036..7150  
 /gene="BRCA1"  
 /number=36  
 7151..7265  
 /gene="BRCA1"  
 /number=37  
 7266..7380  
 /gene="BRCA1"  
 /number=38  
 7381..7495  
 /gene="BRCA1"  
 /number=39  
 7496..7610  
 /gene="BRCA1"  
 /number=40  
 7611..7725  
 /gene="BRCA1"  
 /number=41  
 7726..7840  
 /gene="BRCA1"  
 /number=42  
 7841..7955  
 /gene="BRCA1"  
 /number=43  
 7956..8070  
 /gene="BRCA1"  
 /number=44  
 8071..8185  
 /gene="BRCA1"  
 /number=45  
 8186..8300  
 /gene="BRCA1"  
 /number=46  
 8301..8415  
 /gene="BRCA1"  
 /number=47  
 8416..8530  
 /gene="BRCA1"  
 /number=48  
 8531..8645  
 /gene="BRCA1"  
 /number=49  
 8646..8760  
 /gene="BRCA1"  
 /number=50  
 8761..8875  
 /gene="BRCA1"  
 /number=51  
 8876..8990  
 /gene="BRCA1"  
 /number=52  
 8991..9105  
 /gene="BRCA1"  
 /number=53  
 9106..9220  
 /gene="BRCA1"  
 /number=54  
 9221..9335  
 /gene="BRCA1"  
 /number=55  
 9336..9450  
 /gene="BRCA1"  
 /number=56  
 9451..9565  
 /gene="BRCA1"  
 /number=57  
 9566..9680  
 /gene="BRCA1"  
 /number=58  
 9681..9795  
 /gene="BRCA1"  
 /number=59  
 9796..9910  
 /gene="BRCA1"  
 /number=60  
 9911..10025  
 /gene="BRCA1"  
 /number=61  
 10026..10140  
 /gene="BRCA1"  
 /number=62  
 10141..10255  
 /gene="BRCA1"  
 /number=63  
 10256..10370  
 /gene="BRCA1"  
 /number=64  
 10371..10485  
 /gene="BRCA1"  
 /number=65  
 10486..10600  
 /gene="BRCA1"  
 /number=66  
 10601..10715  
 /gene="BRCA1"  
 /number=67  
 10716..10830  
 /gene="BRCA1"  
 /number=68  
 10831..10945  
 /gene="BRCA1"  
 /number=69  
 10946..11060  
 /gene="BRCA1"  
 /number=70  
 11061..11175  
 /gene="BRCA1"  
 /number=71  
 11176..11290  
 /gene="BRCA1"  
 /number=72  
 11291..11405  
 /gene="BRCA1"  
 /number=73  
 11406..11520  
 /gene="BRCA1"  
 /number=74  
 11521..11635  
 /gene="BRCA1"  
 /number=75  
 11636..11750  
 /gene="BRCA1"  
 /number=76  
 11751..11865  
 /gene="BRCA1"  
 /number=77  
 11866..11980  
 /gene="BRCA1"  
 /number=78  
 11981..12095  
 /gene="BRCA1"  
 /number=79  
 12096..12210  
 /gene="BRCA1"  
 /number=80  
 12211..12325  
 /gene="BRCA1"  
 /number=81  
 12326..12440  
 /gene="BRCA1"  
 /number=82  
 12441..12555  
 /gene="BRCA1"  
 /number=83  
 12556..12670  
 /gene="BRCA1"  
 /number=84  
 12671..12785  
 /gene="BRCA1"  
 /number=85  
 12786..12900  
 /gene="BRCA1"  
 /number=86  
 12901..13015  
 /gene="BRCA1"  
 /number=87  
 13016..13130  
 /gene="BRCA1"  
 /number=88  
 13131..13245  
 /gene="BRCA1"  
 /number=89  
 13246..13360  
 /gene="BRCA1"  
 /number=90  
 13361..13475  
 /gene="BRCA1"  
 /number=91  
 13476..13590  
 /gene="BRCA1"  
 /number=92  
 13591..13705  
 /gene="BRCA1"  
 /number=93  
 13706..13820  
 /gene="BRCA1"  
 /number=94  
 13821..13935  
 /gene="BRCA1"  
 /number=95  
 13936..14050  
 /gene="BRCA1"  
 /number=96  
 14051..14165  
 /gene="BRCA1"  
 /number=97  
 14166..14280  
 /gene="BRCA1"  
 /number=98  
 14281..14395  
 /gene="BRCA1"  
 /number=99  
 14396..14510  
 /gene="BRCA1"  
 /number=100  
 14511..14625  
 /gene="BRCA1"  
 /number=101  
 14626..14740  
 /gene="BRCA1"  
 /number=102  
 14741..14855  
 /gene="BRCA1"  
 /number=103  
 14856..14970  
 /gene="BRCA1"  
 /number=104  
 14971..15085  
 /gene="BRCA1"  
 /number=105  
 15086..15200  
 /gene="BRCA1"  
 /number=106  
 15201..15315  
 /gene="BRCA1"  
 /number=107  
 15316..15430  
 /gene="BRCA1"  
 /number=108  
 15431..15545  
 /gene="BRCA1"  
 /number=109  
 15546..15660  
 /gene="BRCA1"  
 /number=110  
 15661..15775  
 /gene="BRCA1"  
 /number=111  
 15776..15890  
 /gene="BRCA1"  
 /number=112  
 15891..16005  
 /gene="BRCA1"  
 /number=113  
 16006..16120  
 /gene="BRCA1"  
 /number=114  
 16121..16235  
 /gene="BRCA1"  
 /number=115  
 16236..16350  
 /gene="BRCA1"  
 /number=116  
 16351..16465  
 /gene="BRCA1"  
 /number=117  
 16466..16580  
 /gene="BRCA1"  
 /number=118  
 16581..16695  
 /gene="BRCA1"  
 /number=119  
 16696..16810  
 /gene="BRCA1"  
 /number=120  
 16811..16925  
 /gene="BRCA1"  
 /number=121  
 16926..17040  
 /gene="BRCA1"  
 /number=122  
 17041..17155  
 /gene="BRCA1"  
 /number=123  
 17156..17270  
 /gene="BRCA1"  
 /number=124  
 17271..17385  
 /gene="BRCA1"  
 /number=125  
 17386..17500  
 /gene="BRCA1"  
 /number=126  
 17501..17615  
 /gene="BRCA1"  
 /number=127  
 17616..17730  
 /gene="BRCA1"  
 /number=128  
 17731..17845  
 /gene="BRCA1"  
 /number=129  
 17846..17960  
 /gene="BRCA1"  
 /number=130  
 17961..18075  
 /gene="BRCA1"  
 /number=131  
 18076..18190  
 /gene="BRCA1"  
 /number=132  
 18191..18305  
 /gene="BRCA1"  
 /number=133  
 18306..18420  
 /gene="BRCA1"  
 /number=134  
 18421..18535  
 /gene="BRCA1"  
 /number=135  
 18536..18650  
 /gene="BRCA1"  
 /number=136  
 18651..18765  
 /gene="BRCA1"  
 /number=137  
 18766..18880  
 /gene="BRCA1"  
 /number=138  
 18881..18995  
 /gene="BRCA1"  
 /number=139  
 18996..19110  
 /gene="BRCA1"  
 /number=140  
 19111..19225  
 /gene="BRCA1"  
 /number=141  
 19226..19340  
 /gene="BRCA1"  
 /number=142  
 19341..19455  
 /gene="BRCA1"  
 /number=143  
 19456..19570  
 /gene="BRCA1"  
 /number=144  
 19571..19685  
 /gene="BRCA1"  
 /number=145  
 19686..19800  
 /gene="BRCA1"  
 /number=146  
 19801..19915  
 /gene="BRCA1"  
 /number=147  
 19916..20030  
 /gene="BRCA1"  
 /number=148  
 20031..20145  
 /gene="BRCA1"  
 /number=149  
 20146..20260  
 /gene="BRCA1"  
 /number=150  
 20261..20375  
 /gene="BRCA1"  
 /number=151  
 20376..20490  
 /gene="BRCA1"  
 /number=152  
 20491..20605  
 /gene="BRCA1"  
 /number=153  
 20606..20720  
 /gene="BRCA1"  
 /number=154  
 20721..20835  
 /gene="BRCA1"  
 /number=155  
 20836..20950  
 /gene="BRCA1"  
 /number=156  
 20951..21065  
 /gene="BRCA1"  
 /number=157  
 21066..21180  
 /gene="BRCA1"  
 /number=158  
 21181..21295  
 /gene="BRCA1"  
 /number=159  
 21296..21410  
 /gene="BRCA1"  
 /number=160  
 21411..21525  
 /gene="BRCA1"  
 /number=161  
 21526..21640  
 /gene="BRCA1"  
 /number=162  
 21641..21755  
 /gene="BRCA1"  
 /number=163  
 21756..21870  
 /gene="BRCA1"  
 /number=164  
 21871..21985  
 /gene="BRCA1"  
 /number=165  
 21986..22100  
 /gene="BRCA1"  
 /number=166  
 22101..22215  
 /gene="BRCA1"  
 /number=167  
 22216..22330  
 /gene="BRCA1"  
 /number=168  
 22331..22445  
 /gene="BRCA1"  
 /number=169  
 22446..22560  
 /gene="BRCA1"  
 /number=170  
 22561..22675  
 /gene="BRCA1"  
 /number=171  
 22676..22790  
 /gene="BRCA1"  
 /number=172  
 22791..22905  
 /gene="BRCA1"  
 /number=173  
 22906..23020  
 /gene="BRCA1"  
 /number=174  
 23021..23135  
 /gene="BRCA1"  
 /number=175  
 23136..23250  
 /gene="BRCA1"  
 /number=176  
 23251..23365  
 /gene="BRCA1"  
 /number=177  
 23366..23480  
 /gene="BRCA1"  
 /number=178  
 23481..23595  
 /gene="BRCA1"  
 /number=179  
 23596..23710  
 /gene="BRCA1"  
 /number=180  
 23711..23825  
 /gene="BRCA1"  
 /number=181  
 23826..23940  
 /gene="BRCA1"  
 /number=182  
 23941..24055  
 /gene="BRCA1"  
 /number=183  
 24056..24170  
 /gene="BRCA1"  
 /number=184  
 24171..24285  
 /gene="BRCA1"  
 /number=185  
 24286..24400  
 /gene="BRCA1"  
 /number=186  
 24401..24515  
 /gene="BRCA1"  
 /number=187  
 24516..24630  
 /gene="BRCA1"  
 /number=188  
 24631..24745  
 /gene="BRCA1"  
 /number=189  
 24746..24860  
 /gene="BRCA1"  
 /number=190  
 24861..24975  
 /gene="BRCA1"  
 /number=191  
 24976..25090  
 /gene="BRCA1"  
 /number=192  
 25091..25205  
 /gene="BRCA1"  
 /number=193  
 25206..25320  
 /gene="BRCA1"  
 /number=194  
 25321..25435  
 /gene="BRCA1"  
 /number=195  
 25436..25550  
 /gene="BRCA1"  
 /number=196  
 25551..25665  
 /gene="BRCA1"  
 /number=197  
 25666..25780  
 /gene="BRCA1"  
 /number=198  
 25781..25895  
 /gene="BRCA1"  
 /number=199  
 25896..26010  
 /gene="BRCA1"  
 /number=200  
 26011..26125  
 /gene="BRCA1"  
 /number=201  
 26126..26240  
 /gene="BRCA1"  
 /number=202  
 26241..26355  
 /gene="BRCA1"  
 /number=203  
 26356..26470  
 /gene="BRCA1"  
 /number=204  
 26471..26585  
 /gene="BRCA1"  
 /number=205  
 26586..26700  
 /gene="BRCA1"  
 /number=206  
 26701..26815  
 /gene="BRCA1"  
 /number=207  
 26816..26930  
 /gene="BRCA1"  
 /number=208  
 26931..27045  
 /gene="BRCA1"  
 /number=209  
 27046..27160  
 /gene="BRCA1"  
 /number=210  
 27161..27275  
 /gene="BRCA1"  
 /number=211  
 27276..27390  
 /gene="BRCA1"  
 /number=212  
 27391..27505  
 /gene="BRCA1"  
 /number=213  
 27506..27620  
 /gene="BRCA1"  
 /number=214  
 27621..27735  
 /gene="BRCA1"  
 /number=215  
 27736..27850  
 /gene="BRCA1"  
 /number=216  
 27851..27965  
 /gene="BRCA1"  
 /number=217  
 27966..28080  
 /gene="BRCA1"  
 /number=218  
 28081..28195  
 /gene="BRCA1"  
 /number=219  
 28196..28310  
 /gene="BRCA1"  
 /number=220  
 28311..28425  
 /gene="BRCA1"  
 /number=221  
 28426..28540  
 /gene="BRCA1"  
 /number=222  
 28541..28655  
 /gene="BRCA1"  
 /number=223  
 28656..28770  
 /gene="BRCA1"  
 /number=224  
 28771..28885  
 /gene="BRCA1"  
 /number=225  
 28886..29000  
 /gene="BRCA1"  
 /number=226  
 29001..29115  
 /gene="BRCA1"  
 /number=227  
 29116..29230  
 /gene="BRCA1"  
 /number=228  
 29231..29345  
 /gene="BRCA1"  
 /number=229  
 29346..29460  
 /gene="BRCA1"  
 /number=230  
 29461..29575  
 /gene="BRCA1"  
 /number=231  
 29576..29690  
 /gene="BRCA1"  
 /number=232  
 29691..29805  
 /gene="BRCA1"  
 /number=233  
 29806..29920  
 /gene="BRCA1"  
 /number=234  
 29921..30035  
 /gene="BRCA1"  
 /number=235  
 30036..30150  
 /gene="BRCA1"  
 /number=236  
 30151..30265  
 /gene="BRCA1"  
 /number=237  
 30266..30380  
 /gene="BRCA1"  
 /number=238  
 30381..30495  
 /gene="BRCA1"  
 /number=239  
 30496..30610  
 /gene="BRCA1"  
 /number=240  
 30611..30725  
 /gene="BRCA1"  
 /number=241  
 30726..30840  
 /gene="BRCA1"  
 /number=242  
 30841..30955  
 /gene="BRCA1"  
 /number=243  
 30956..31070  
 /gene="BRCA1"  
 /number=244  
 31071..31185  
 /gene="BRCA1"  
 /number=245  
 31186..31300  
 /gene="BRCA1"  
 /number=246  
 31301..31415  
 /gene="BRCA1"  
 /number=247  
 31416..31530  
 /gene="BRCA1"  
 /number=248  
 31531..31645  
 /gene="BRCA1"  
 /number=249  
 31646..31760  
 /gene="BRCA1"  
 /number=250  
 31761..31875  
 /gene="BRCA1"  
 /number=251  
 31876..31990  
 /gene="BRCA1"  
 /number=252  
 31991..32105  
 /gene="BRCA1"  
 /number=253  
 32106..32220  
 /gene="BRCA1"  
 /number=254  
 32221..32335  
 /gene="BRCA1"  
 /number=255  
 32336..32450  
 /gene="BRCA1"  
 /number=256  
 32451..32565  
 /gene="BRCA1"  
 /number=257  
 32566..32680  
 /gene="BRCA1"  
 /number=258  
 32681..32795  
 /gene="BRCA1"  
 /number=259  
 32796..32910  
 /gene="BRCA1"  
 /number=260  
 32911..33025  
 /gene="BRCA1"  
 /number=261  
 33026..33140  
 /gene="BRCA1"  
 /number=262  
 33141..33255  
 /gene="BRCA1"  
 /number=263  
 33256..33370  
 /gene="BRCA1"  
 /number=264  
 33371..33485  
 /gene="BRCA1"  
 /number=265  
 33486..33600  
 /gene="BRCA1"  
 /number=266  
 33601..33715  
 /gene="BRCA1"  
 /number=267  
 33716..33830  
 /gene="BRCA1"  
 /number=268  
 33831..33945  
 /gene="BRCA1"  
 /number=269  
 33946..34060  
 /gene="BRCA1"  
 /number=270  
 34061..34175  
 /gene="BRCA1"  
 /number=271  
 34176..34290  
 /gene="BRCA1"  
 /number=272  
 34291..34405  
 /gene="BRCA1"  
 /number=273  
 34406..34520  
 /gene="BRCA1"  
 /number=274  
 34521..34635  
 /gene="BRCA1"  
 /number=275  
 34636..34750  
 /gene="BRCA1"  
 /number=276  
 34751..34865  
 /gene="BRCA1"  
 /number=277  
 34866..34980  
 /gene="BRCA1"  
 /number=278  
 34981..35095  
 /gene="BRCA1"  
 /number=279  
 35096..35210  
 /gene="BRCA1"  
 /number=280  
 35211..35325  
 /gene="BRCA1"  
 /number=281  
 35326..35440  
 /gene="BRCA1"  
 /number=282  
 35441..35555  
 /gene="BRCA1"  
 /number=283  
 35556..35670  
 /gene="BRCA1"  
 /number=284  
 35671..35785  
 /gene="BRCA1"  
 /number=285  
 35786..35900  
 /gene="BRCA1"  
 /number=286  
 35901..36015  
 /gene="BRCA1"  
 /number=287  
 36016..36130  
 /gene="BRCA1"  
 /number=288  
 36131..36245  
 /gene="BRCA1"  
 /number=289  
 36246..36360  
 /gene="BRCA1"  
 /number=290  
 36361..36475  
 /gene="BRCA1"  
 /number=291  
 36476..36590  
 /gene="BRCA1"  
 /number=292  
 36591..36705  
 /gene="BRCA1"  
 /number=293  
 36706..36820  
 /gene="BRCA1"  
 /number=294  
 36821..36935  
 /gene="BRCA1"  
 /number=295  
 36936..37050  
 /gene="BRCA1"  
 /number=296  
 37051..37165  
 /gene="BRCA1"  
 /number=297  
 37166..37280  
 /gene="BRCA1"  
 /number=298  
 37281..37395  
 /gene="BRCA1"  
 /number=299  
 37396..37510  
 /gene="BRCA1"  
 /number=300  
 37511..37625  
 /gene="BRCA1"  
 /number=301  
 37626..37740  
 /gene="BRCA1"  
 /number=302  
 37741..37855  
 /gene="BRCA1"  
 /number=303  
 37856..37970  
 /gene="BRCA1"  
 /number=304  
 37971..38085  
 /gene="BRCA1"  
 /number=305  
 38086..38200  
 /gene="BRCA1"  
 /number=306  
 38201..38315  
 /gene="BRCA1"  
 /number=307  
 38316..38430  
 /gene="BRCA1"  
 /number=308  
 38431..38545  
 /gene="BRCA1"  
 /number=309  
 38546..38660  
 /gene="BRCA1"  
 /number=310  
 38661..38775  
 /gene="BRCA1"  
 /number=311  
 38776..38890  
 /gene="BRCA1"  
 /number=312  
 38891..39005  
 /gene="BRCA1"  
 /number=313  
 39006..39120  
 /gene="BRCA1"  
 /number=314  
 39121..39235  
 /gene="BRCA1"  
 /number=315  
 39236..39350  
 /gene="BRCA1"  
 /number=316  
 39351..39465  
 /gene="BRCA1"  
 /number=317  
 39466..39580  
 /gene="BRCA1"  
 /number=318  
 39581..39695  
 /gene="BRCA1"  
 /number=319  
 39696..39810  
 /gene="BRCA1"  
 /number=320  
 39811..39925  
 /gene="BRCA1"  
 /number=321  
 39926..40040  
 /gene="BRCA1"  
 /number=322  
 40041..40155  
 /gene="BRCA1"  
 /number=323  
 40156..40270  
 /gene="BRCA1"  
 /number=324  
 40271..40385  
 /gene="BRCA1"  
 /number=325  
 40386..40500  
 /gene="BRCA1"  
 /number=326  
 40501..40615  
 /gene="BRCA1"  
 /number=327  
 40616..40730  
 /gene="BRCA1"  
 /number=328  
 40731..40845  
 /gene="BRCA1"  
 /number=329  
 40846..40960  
 /gene="BRCA1"  
 /number=330  
 40961..41075  
 /gene="BRCA1"  
 /number=331  
 41076..41190  
 /gene="BRCA1"

QY 1021 AGCTGAATTCGTGTAATAAAGCAAAAGCCTGGCTTAGCAGAGCCAACTAACAGAT 1080  
| | | | |  
Db 1021 AGCTGAATTCGTGTAATAAAGCAAAAGCCTGGCTTAGCAGAGCCAACTAACAGAT 1080  
QY 1081 GGGCTGGAAGTAGAGAAACATGTAATGATAGGGGAGCTCCACAGACGAAAAAGGTAG 1140  
| | | | |  
Db 1081 GGGCTGGAAGTAGAGAAACATGTAATGATAGGGGAGCTCCACAGACGAAAAAGGTAG 1140  
QY 1141 ATCTGAATCCTGATCCCTGCTGTGAGAGAAAAGAAATGGAATAAGCAAACTCCATGCT 1200  
| | | | |  
Db 1141 ATCTGAATCCTGATCCCTGCTGTGAGAGAAAAGAAATGGAATAAGCAAACTCCATGCT 1200  
QY 1201 CAGAGATCCTGAGAGTACTGGAAGATGTTCTTGATTAACACTAAATAGCAGACTTCAGA 1260  
| | | | |  
Db 1201 CAGAGATCCTGAGAGTACTGGAAGATGTTCTTGATTAACACTAAATAGCAGACTTCAGA 1260  
QY 1261 AGTTAATAGAGTGTTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1320  
| | | | |  
Db 1261 AGTTAATAGAGTGTTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1320  
QY 1321 GGGAGTCTGGAATCAAAATGCCAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1380  
| | | | |  
Db 1321 GGGAGTCTGGAATCAAAATGCCAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1380  
QY 1381 AATATTCCTGCTCTTCTGAGAGAAAATGACTTACTGCGCAGCTGATCCTCATGAGGCTTTAA 1440  
| | | | |  
Db 1381 AATATTCCTGCTCTTCTGAGAGAAAATGACTTACTGCGCAGCTGATCCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTAGAAGAGTCACTCCAAATCAGTAGAGATATATTTGAAGCAAAATAT 1500  
| | | | |  
Db 1441 TATGTAAAGTAGAAGAGTCACTCCAAATCAGTAGAGATATATTTGAAGCAAAATAT 1500  
QY 1501 TTGGAAAAACCTATCGGAAGAAAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAAGAAATC 1560  
| | | | |  
Db 1501 TTGGAAAAACCTATCGGAAGAAAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAAGAAATC 1560  
QY 1561 TAATATAGAGACATTTGTTTACTAGACCCACAGATATTAACAAGAGCTCCCTCACAATAA 1620  
| | | | |  
Db 1561 TAATATAGAGACATTTGTTTACTAGACCCACAGATATTAACAAGAGCTCCCTCACAATAA 1620  
QY 1621 AATTAAGGCTAAAGAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680  
| | | | |  
Db 1621 AATTAAGGCTAAAGAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAATGATTAATCAGGGAACCTAACCAAAAGGAGC 1740  
| | | | |  
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAATGATTAATCAGGGAACCTAACCAAAAGGAGC 1740  
QY 1741 AGAATGCTCAAGTGAATATTAATAGTGTGATGAGAAATTAACAAAAAGTGAT 1800  
| | | | |  
Db 1741 AGAATGCTCAAGTGAATATTAATAGTGTGATGAGAAATTAACAAAAAGTGAT 1800  
QY 1801 CTATTCAGATGAGAAAAATCTTAACCCAAATGAAATCATCTCGAAAAAGAAATCTGCTTTAA 1860  
| | | | |  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCCAAATGAAATCATCTCGAAAAAGAAATCTGCTTTAA 1860  
QY 1861 AAACGAAAGCTGAACCTATTAAGCAGCAGTATAAGCAATATGGAATCGAATTAATATATCC 1920  
| | | | |  
Db 1861 AAACGAAAGCTGAACCTATTAAGCAGCAGTATAAGCAATATGGAATCGAATTAATATATCC 1920  
QY 1921 ACAATTCAAAAGCACCCTTAATAAAGAAATAGGCTGAGAGAGAGTCTTACCAGAGCATATTC 1980  
| | | | |  
Db 1921 ACAATTCAAAAGCACCCTTAATAAAGAAATAGGCTGAGAGAGAGTCTTACCAGAGCATATTC 1980  
QY 1981 ATGCGCTGAAGTACTAGTACAGTAAATCTAAGCCACCTAATTTACTGATTCGAA 2040  
| | | | |  
Db 1981 ATGCGCTGAAGTACTAGTACAGTAAATCTAAGCCACCTAATTTACTGATTCGAA 2040  
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGCCAGTCA 2100  
| | | | |  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGCCAGTCA 2100

QY 2101 GGCACAGCAGAAACCTTACAACTCATGGAAGTAAAGAACTGCAACAGGAGCCAGAAAGA 2160  
| | | | |  
Db 2101 GGCACAGCAGAAACCTTACAACTCATGGAAGTAAAGAACTGCAACAGGAGCCAGAAAGA 2160  
QY 2161 GTACACAGCAGAAATGACAGCAAGTAAAGAGCATGACAGGATACCTTCCAGAGCTGA 2220  
| | | | |  
Db 2161 GTACACAGCAGAAATGACAGCAAGTAAAGAGCATGACAGGATACCTTCCAGAGCTGA 2220  
QY 2221 AGTTAACAATGACACCTGGTCTTTTACTAAGTGTCAATATACAGTGAACCTTAAGAAAT 2280  
| | | | |  
Db 2221 AGTTAACAATGACACCTGGTCTTTTACTAAGTGTCAATATACAGTGAACCTTAAGAAAT 2280  
QY 2281 TTGTCAATCCTGCTTCCAGAGAGAAAAAGAGAAACTGAAAAAGTAAAGTGT 2340  
| | | | |  
Db 2281 TTGTCAATCCTGCTTCCAGAGAGAAAAAGAGAAACTGAAAAAGTAAAGTGT 2340  
QY 2341 CTAAATATCTGAGAACCCCAAAAGTCTCATGTTAAGTGAAGAAAGGTTTGCAAACTG 2400  
| | | | |  
Db 2341 CTAAATATCTGAGAACCCCAAAAGTCTCATGTTAAGTGAAGAAAGGTTTGCAAACTG 2400  
QY 2401 AAAGATCTGTAGAGAGTACAGATATTTGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2460  
| | | | |  
Db 2401 AAAGATCTGTAGAGAGTACAGATATTTGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2460  
QY 2461 AAAGATCTGTTACTGGAAGTACAGTCTAGGAGAGCCAAACGAAACCAATTAAT 2520  
| | | | |  
Db 2461 AAAGATCTGTTACTGGAAGTACAGTCTAGGAGAGCCAAACGAAACCAATTAAT 2520  
QY 2521 GTGTGAGTCAAGTGTGACATTTGAAACCCCAAGGAGCTAATCATGAGTGTTCCAAAG 2580  
| | | | |  
Db 2521 GTGTGAGTCAAGTGTGACATTTGAAACCCCAAGGAGCTAATCATGAGTGTTCCAAAG 2580  
QY 2581 ATAAATAGAAATGACACAGAAAGCCTTAAGTATCCATTGGACATGAAGTTAACACAGTC 2640  
| | | | |  
Db 2581 ATAAATAGAAATGACACAGAAAGCCTTAAGTATCCATTGGACATGAAGTTAACACAGTC 2640  
QY 2641 GGGAAACAAGCATTAATAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700  
| | | | |  
Db 2641 GGGAAACAAGCATTAATAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700  
QY 2701 TCAAGTTTCAAAAGGCCAGTCAATTTGCTGTTTCAAAATCCAGAAAGTGAAGAGAG 2760  
| | | | |  
Db 2701 TCAAGTTTCAAAAGGCCAGTCAATTTGCTGTTTCAAAATCCAGAAAGTGAAGAGAG 2760  
QY 2761 AATGTCAACATTCCTGCTCCACCTCTGGGCTTTAAGAAACCAATGTCAAAAGTCACTT 2820  
| | | | |  
Db 2761 AATGTCAACATTCCTGCTCCACCTCTGGGCTTTAAGAAACCAATGTCAAAAGTCACTT 2820  
QY 2821 TTGATGTGAACAAAGAGAAAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC 2880  
| | | | |  
Db 2821 TTGATGTGAACAAAGAGAAAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC 2880  
QY 2881 AGACAGTAAATATCACTCAGGCTTCTGTTGTTGTCAGAAAGATGAAGCAGTTGATA 2940  
| | | | |  
Db 2881 AGACAGTAAATATCACTCAGGCTTCTGTTGTTGTCAGAAAGATGAAGCAGTTGATA 2940  
QY 2941 ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTAGAGGCA 3000  
| | | | |  
Db 2941 ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTAGAGGCA 3000  
QY 3001 AGGAAACTGGAAGTCAATTAATCAAAATGAGACTTTTACAAAACCCATATCAGATAC 3060  
| | | | |  
Db 3001 AGGAAACTGGAAGTCAATTAATCAAAATGAGACTTTTACAAAACCCATATCAGATAC 3060  
QY 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAATTAATGAAGAAATCTGTAGAGG 3120  
| | | | |  
Db 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAATTAATGAAGAAATCTGTAGAGG 3120  
QY 3121 AAAACTTTGAGAAACATTCATGTCACCTGTAAGAGAAATGGAAGATGAGACATTCGA 3180  
| | | | |  
Db 3121 AAAACTTTGAGAAACATTCATGTCACCTGTAAGAGAAATGGAAGATGAGACATTCGA 3180  
QY 3181 GTACAGTGAAGCAATTAAGCCGTAAATACATTAAGAGAAATGTTTTTAAGAGCCAGCT 3240

|||||  
Db 3181 GTACAGTACGACATTTAGCCGTAAATACATTAGAGAAAATGTTTTAAAGAACCCAGCT 3240  
Qy 3241 CAACCAATATTAAATGAAGTAGTTCACAGTACTAATGAAGTGGCTCCAGTATTATGAAA 3300  
Db 3241 CAACCAATATTAAATGAAGTAGTTCACAGTACTAATGAAGTGGCTCCAGTATTATGAAA 3300  
Qy 3301 TAGGTTCCAGTATGAGAAAACATTCAAGCAGACAGTAGTAGAACAAGAGGCCAAAATTGA 3360  
Db 3301 TAGGTTCCAGTATGAGAAAACATTCAAGCAGACAGTAGTAGAACAAGAGGCCAAAATTGA 3360  
Qy 3361 ATGCTATGCTTAGAGTTAGGGGTTTTGCAACCTGAGTCTATAAACAAGTCTTCTGGAA 3420  
Db 3361 ATGCTATGCTTAGAGTTAGGGGTTTTGCAACCTGAGTCTATAAACAAGTCTTCTGGAA 3420  
Qy 3421 GTAATTGATACATCTCGAATAATAAAAAGCAAGATATGAAGAATGTTAGACTGTTA 3480  
Db 3421 GTAATTGATACATCTCGAATAATAAAAAGCAAGATATGAAGAATGTTAGACTGTTA 3480  
Qy 3481 ATACAGATTTTCTTCATATCTGATTTCAATTAACCTTGAACAGCCTTATGGGAAGTATC 3540  
Db 3481 ATACAGATTTTCTTCATATCTGATTTCAATTAACCTTGAACAGCCTTATGGGAAGTATC 3540  
Qy 3541 ATGATCTCAGAGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGAGTAATTAAG 3600  
Db 3541 ATGATCTCAGAGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGAGTAATTAAG 3600  
Qy 3601 AAGTACTAGTTTGTCTGAAAATACATTAAGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
Db 3601 AAGTACTAGTTTGTCTGAAAATACATTAAGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
Qy 3661 TCCGAAAGAGAGACTTATGACGAGAGTCTAGCCCTTACACCATACACATTTGGCTCAG 3720  
Db 3661 TCCGAAAGAGAGACTTATGACGAGAGTCTAGCCCTTACACCATACACATTTGGCTCAG 3720  
Qy 3721 GTTACCGAGAGGGGCCAAGAAATTAGAGTCTGAGAAAGAACTTATCTGTAGAGATG 3780  
Db 3721 GTTACCGAGAGGGGCCAAGAAATTAGAGTCTGAGAAAGAACTTATCTGTAGAGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTCCAACTTGTATTTGGTAAAGTAAACAAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTCCAACTTGTATTTGGTAAAGTAAACAAATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCAATGACACGCTGCTACCGAGTCTGTCTAAACACAGAGAGATTTAT 3900  
Db 3841 CTACTAGGCAATGACACGCTGCTACCGAGTCTGTCTAAACACAGAGAGATTTAT 3900  
Qy 3901 TATATGGAAGATAGCTTAAATAGACTGACATACAGAGTAAATTTGSCAAAGGCAATCTC 3960  
Db 3901 TATATGGAAGATAGCTTAAATAGACTGACATACAGAGTAAATTTGSCAAAGGCAATCTC 3960  
Qy 3961 AGAAGCATCACCCTTAGTGAAGAAACAAATGTCTGCTAGCTTTCTTCTTCTCAGAGTCA 4020  
Db 3961 AGAAGCATCACCCTTAGTGAAGAAACAAATGTCTGCTAGCTTTCTTCTTCTCAGAGTCA 4020  
Qy 4021 GTGATTTGGAAGACTTGACTGCAAAATACAAACACCCAGAGATCTTTCTGATTTGTTCTT 4080  
Db 4021 GTGATTTGGAAGACTTGACTGCAAAATACAAACACCCAGAGATCTTTCTGATTTGTTCTT 4080  
Qy 4081 CCAAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTAGAGTACAAAGAAATGG 4140  
Db 4081 CCAAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTAGAGTACAAAGAAATGG 4140  
Qy 4141 TTTGAGATGATGAGAAAGAGAGAAAGGGCTTGAAGAAATATCAAGAAAGAGCAAAAGCA 4200  
Db 4141 TTTGAGATGATGAGAAAGAGAGAAAGGGCTTGAAGAAATATCAAGAAAGAGCAAAAGCA 4200  
Qy 4201 TGGATTTCAAATTTAGGTGAGACAGCATTTGGGTGTAGAGTGAACAAGCCTCTCTGAG 4260  
Db 4201 TGGATTTCAAATTTAGGTGAGACAGCATTTGGGTGTAGAGTGAACAAGCCTCTCTGAG 4260  
Qy 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTAACACACAGAGGATACCATGC 4320  
|||||

Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTAACCATCTCAGAGAGGATACCATGC 4320  
Qy 4321 AACATAACCTGATTAAGACCTCCAGCAGAGAAATGGCTGAACATGAAAGCTGTGTAGACAGC 4380  
Db 4321 AACATAACCTGATTAAGACCTCCAGCAGAGAAATGGCTGAACATGAAAGCTGTGTAGACAGC 4380  
Qy 4381 ATGGGAGCCAGCCTTCTTAACAGCTACCTTTCATCATTAAGTACTCTTCTGCTTAGG 4440  
Db 4381 ATGGGAGCCAGCCTTCTTAACAGCTACCTTTCATCATTAAGTACTCTTCTGCTTAGG 4440  
Qy 4441 ACCGGAAGATCCAGAACAAAGCAGATCAGAAAAAGAGATTAATTAATCTCAGAAAAATGA 4500  
Db 4441 ACCGGAAGATCCAGAACAAAGCAGATCAGAAAAAGAGATTAATTAATCTCAGAAAAATGA 4500  
Qy 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTGTAGTGTCTG 4560  
Db 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTGTAGTGTCTG 4560  
Qy 4561 CAGATTAATTTTACAGTAAATAATTAAGAACACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
Db 4561 CAGATTAATTTTACAGTAAATAATTAAGAACACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
Qy 4621 GCCCATATTAGATGATGAGTGTACATGACAGTGTCTCTGGAGTCTTCAGAAATGAA 4680  
Db 4621 GCCCATATTAGATGATGAGTGTACATGACAGTGTCTCTGGAGTCTTCAGAAATGAA 4680  
Qy 4681 ACTACCATCTCAAGAGAGCTCTTAAGTGTGTGATGTGAGAGACCAACAGCTGAGAG 4740  
Db 4681 ACTACCATCTCAAGAGAGAGCTCTTAAGTGTGTGATGTGAGAGACCAACAGCTGAGAG 4740  
Qy 4741 AGTCTGGGCCACACAGATTTGACGGAAACATCTTACTTCCAAAGCAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACACAGATTTGACGGAAACATCTTACTTCCAAAGCAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTATGACCCGAATCTGATCTCTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTATGACCCGAATCTGATCTCTG 4860  
Qy 4861 AAGACAGAGCCCAAGAGTCACTGCTGTGGCAACATACCATCTTCAACCTCTGATTTGA 4920  
Db 4861 AAGACAGAGCCCAAGAGTCACTGCTGTGGCAACATACCATCTTCAACCTCTGATTTGA 4920  
Qy 4921 AAGTCCCAATGAAGATTTGACAGATCTGCCAGAGTCCAGCTGCTGCTATATCTG 4980  
Db 4921 AAGTCCCAATGAAGATTTGACAGATCTGCCAGAGTCCAGCTGCTGCTATATCTG 4980  
Qy 4981 ATACTGCTGGTAAATAGCAATGGAAGAAAGTGTGACAGAGGAGAACCCGAATTTGACAG 5040  
Db 4981 ATACTGCTGGTAAATAGCAATGGAAGAAAGTGTGACAGAGGAGAACCCGAATTTGACAG 5040  
Qy 5041 CTTCAACAGAAAGGGTCAACAAAAGAAATGTCAATGTGTGTGCTGAGCTGACCCAGAG 5100  
Db 5041 CTTCAACAGAAAGGGTCAACAAAAGAAATGTCAATGTGTGTGCTGAGCTGACCCAGAG 5100  
Qy 5101 AATTTATGCTGCTGTACAAATTTGCCAGAAACACACATCACTTTACTATATTA 5160  
Db 5101 AATTTATGCTGCTGTACAAATTTGCCAGAAACACACATCACTTTACTATATTA 5160  
Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGAACGGGACAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGAACGGGACAC 5220  
Qy 5221 TGAATATTTTCTAGAAATTCGGGAGAGAAATGGTAGTTAGCTATTCTGGGTGACC 5280  
Db 5221 TGAATATTTTCTAGAAATTCGGGAGAGAAATGGTAGTTAGCTATTCTGGGTGACC 5280  
Qy 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTG 5340  
Db 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTG 5340  
Qy 5341 TCAATGGAAGAAACCAAGAGTCCAAAGGAGAGAGAGATCCAGAGAGAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACCAAGAGTCCAAAGGAGAGAGAGATCCAGAGAGAAAGATCT 5400

[illegible]

Db 1381 AATATTCTGCTTCTCAGAGAAATAGACTTGTGCGCCAGTATCTCATGAGCTTTAA 1440  
Oy 1441 TATGTAAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATATTTGAAGCAAAATAT 1500  
Db 1441 TATGTAAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATATTTGAAGCAAAATAT 1500  
Oy 1501 TTGGGAAAACCTATCGGAGAAAGGCAAGCCTCCCACTAAAGCCATGTAACTGAAATC 1560  
Db 1501 TTGGGAAAACCTATCGGAGAAAGGCAAGCCTCCCACTAAAGCCATGTAACTGAAATC 1560  
Oy 1561 TAATTATAGAGCATTTGTTACTGAGCCACAGATATATACAGAGGCTCCCTCACAAATA 1620  
Db 1561 TAATTATAGAGCATTTGTTACTGAGCCACAGATATATACAGAGGCTCCCTCACAAATA 1620  
Oy 1621 AATTAAGCGTAAAAGAGAGACCTACATCAGGCTTCATCCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGCGTAAAAGAGAGACCTACATCAGGCTTCATCCTGAGGATTTTATCAAGAAAG 1680  
Oy 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATATTAATCAGGAACTAAACCAAGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATATTAATCAGGAACTAAACCAAGGAGC 1740  
Oy 1741 AGAATGTCAGTGAATGATATTTACTAATATGTCATGAGATATAACCAAGGAGAT 1800  
Db 1741 AGAATGTCAGTGAATGATATTTACTAATATGTCATGAGATATAACCAAGGAGAT 1800  
Oy 1801 CTATTGAGATGAGAAAAATCTTAACCCATAGAAATCAGCTCGAAAAAGATCTGTTTCA 1860  
Db 1801 CTATTGAGATGAGAAAAATCTTAACCCATAGAAATCAGCTCGAAAAAGATCTGTTTCA 1860  
Oy 1861 AAACGAAAGCTAACCCTATTAACAGCAGATATTAAGCAATATGGAATCGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTAACCCTATTAACAGCAGATATTAAGCAATATGGAATCGAATTAATATCC 1920  
Oy 1921 ACAATTCAAAAGCACCCTAAAAGATAGGCTGAGGAGAACTCTACAGGAGATATTC 1980  
Db 1921 ACAATTCAAAAGCACCCTAAAAGATAGGCTGAGGAGAACTCTACAGGAGATATTC 1980  
Oy 1981 ATGCGCTTGAACTAGTACTAGTAGAAATCTAAGCCACCTAATTTGTAAGTATTCAAA 2040  
Db 1981 ATGCGCTTGAACTAGTACTAGTAGAAATCTAAGCCACCTAATTTGTAAGTATTCAAA 2040  
Oy 2041 TTGATATGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTACACCAATGCCAGTCA 2100  
Db 2041 TTGATATGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTACACCAATGCCAGTCA 2100  
Oy 2101 GGCACAGAGAAACCTACAACTCATGAGAGTAAAGAACTGCAACTGGAGCCAGAAAGA 2160  
Db 2101 GGCACAGAGAAACCTACAACTCATGAGAGTAAAGAACTGCAACTGGAGCCAGAAAGA 2160  
Oy 2161 GTAAACAGCCAAATGAGACAGACAAATGAAAGACATGACAGCATCTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAGACAGACAAATGAAAGACATGACAGCATCTTCCAGAGCTGA 2220  
Oy 2221 AGTTAAACAAATCAGCTGTTCTTTACTCAATGTTTCAAAATCCAGTGAATTAAGAAAT 2280  
Db 2221 AGTTAAACAAATCAGCTGTTCTTTACTCAATGTTTCAAAATCCAGTGAATTAAGAAAT 2280  
Oy 2281 TTGTCATATCTGAGCTTCCCAAGAGAAAGAAAGAGAACTAGAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCATATCTGAGCTTCCCAAGAGAAAGAAAGAGAACTAGAAACAGTTAAAGTGT 2340  
Oy 2341 CTAAATATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAGAACTG 2400  
Db 2341 CTAAATATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAGAACTG 2400  
Oy 2401 AAAGATCTGTAAGAGTAGACATATTTCAATTTGTAAGTGAAGTATTTGAGCACTGAG 2460  
Db 2401 AAAGATCTGTAAGAGTAGACATATTTCAATTTGTAAGTGAAGTATTTGAGCACTGAG 2460  
Oy 2461 AAAGATCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2520  
Db 2461 AAAGATCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2520

Oy 2521 GTGTAGTCACTGTGACACCATTTGAAAAACCCCAAGGACATATTCAGTGTGTTCCAAAG 2580  
Db 2521 GTGTAGTCACTGTGACACCATTTGAAAAACCCCAAGGACATATTCAGTGTGTTCCAAAG 2580  
Oy 2581 ATAAATGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATTAATTAACCACTG 2640  
Db 2581 ATAAATGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATTAATTAACCACTG 2640  
Oy 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTGATGCTCAGATTTGCAATATACAT 2700  
Db 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTGATGCTCAGATTTGCAATATACAT 2700  
Oy 2701 TCAAGTTTCAAAAGCGCAGTCAATTTGCTGTTTCAATTCAGAAATGCAAGAGAG 2760  
Db 2701 TCAAGTTTCAAAAGCGCAGTCAATTTGCTGTTTCAATTCAGAAATGCAAGAGAG 2760  
Oy 2761 AATGTCAAACATCTCTCTCCCACTCTGGGCTCTTAAAGAAAGTCCCAAAAGTCACTT 2820  
Db 2761 AATGTCAAACATCTCTCTCCCACTCTGGGCTCTTAAAGAAAGTCCCAAAAGTCACTT 2820  
Oy 2821 TTGAATGTGAACAAAAGAGAAAGAAATCAAGGAAAGATGAGTCTAATATCAAGCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAAGAGAAAGAAATCAAGGAAAGATGAGTCTAATATCAAGCTGTAC 2880  
Oy 2881 AGACAGTTAATATCATCTCAGGCTTCTGTTGTTGTCAGAAAGATTAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCATCTCAGGCTTCTGTTGTTGTCAGAAAGATTAAGCCAGTTGATA 2940  
Oy 2941 ATGCCAAATGATATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
Db 2941 ATGCCAAATGATATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
Oy 3001 AGCAATCTGAGCTCATCTCTCAAAATTAACATGAGCTTTCAAAACCATATCTATATC 3060  
Db 3001 AGCAATCTGAGCTCATCTCTCAAAATTAACATGAGCTTTCAAAACCATATCTATATC 3060  
Oy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAATGTAAGAAATCTGCTAGAGG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAATGTAAGAAATCTGCTAGAGG 3120  
Oy 3121 AAACTTTGAGGACATTCATATGTCAGTGAAGAAAGGAAATGAGAAATGAGAACTTCAA 3180  
Db 3121 AAACTTTGAGGACATTCATATGTCAGTGAAGAAAGGAAATGAGAAATGAGAACTTCAA 3180  
Oy 3181 GTACAGTGAACAAATTCAGGCTAATTAACATTAAGAAATGTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAACAAATTCAGGCTAATTAACATTAAGAAATGTTTAAAGAGCCAGCT 3240  
Oy 3241 CAAGCAATATTAATGAAAGTGAAGTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAAGTGAAGTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Oy 3301 TAGGTTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3360  
Db 3301 TAGGTTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3360  
Oy 3361 ATGCTATGCTTAGANTTAGGGGTTTTCAGAACTGAGGCTTATTAACCAAGTCTTCTGTGAA 3420  
Db 3361 ATGCTATGCTTAGANTTAGGGGTTTTCAGAACTGAGGCTTATTAACCAAGTCTTCTGTGAA 3420  
Oy 3421 GTAATTTGAGCATCTGTAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGACTGTTA 3480  
Db 3421 GTAATTTGAGCATCTGTAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGACTGTTA 3480  
Oy 3481 ATACAGATTTTCTCTCATATCTGATTTGATTAAGTGAAGCAGCTATGGAAGTACTC 3540  
Db 3481 ATACAGATTTTCTCTCATATCTGATTTGATTAAGTGAAGCAGCTATGGAAGTACTC 3540  
Oy 3541 ATGATCTCAGGTTTGTCTAGAGACACTGATGACCTTGTGATGATGATGATGATGATGAT 3600  
Db 3541 ATGATCTCAGGTTTGTCTAGAGACACTGATGACCTTGTGATGATGATGATGATGATGAT 3600

QY 3601 AAGATCTAGTTTGTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTGTAGCAAAAGG 3660  
| | | | |  
Db 3601 AAGATCTAGTTTGTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTGTAGCAAAAGG 3660  
QY 3661 TCCGAAAGAGAGGCTTACGAGAGTCTAGCCCTTCAACCCATACACATTTGGCTCAG 3720  
| | | | |  
Db 3661 TCCGAAAGAGAGGCTTACGAGAGTCTAGCCCTTCAACCCATACACATTTGGCTCAG 3720  
QY 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTAGAGAGAACTTATCTAGTAGAGAG 3780  
| | | | |  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTAGAGAGAACTTATCTAGTAGAGAG 3780  
QY 3781 AAGACTTCCCTGCTTCCACACTTGTATTTGGTAAAGTAAACATATACCTTCTCAGT 3840  
| | | | |  
Db 3781 AAGACTTCCCTGCTTCCACACTTGTATTTGGTAAAGTAAACATATACCTTCTCAGT 3840  
QY 3841 CTACAGGACATGACACCGGTGTACCGAGTGTCTCTAAGAACACAGAGAGAAATTAAT 3900  
| | | | |  
Db 3841 CTACAGGACATGACACCGGTGTACCGAGTGTCTCTAAGAACACAGAGAGAAATTAAT 3900  
QY 3901 TATCATTTGAGAAATAGCTTAAATGACTGTACGTACCAAGTAAATATTGCCAAGGCAATCTC 3960  
| | | | |  
Db 3901 TATCATTTGAGAAATAGCTTAAATGACTGTACGTACCAAGTAAATATTGCCAAGGCAATCTC 3960  
QY 3961 AGGAACATCACCTTAGTGAGAAACAAATGTCTGCTAGCTTGTCTTCTACAGTGA 4020  
| | | | |  
Db 3961 AGGAACATCACCTTAGTGAGAAACAAATGTCTGCTAGCTTGTCTTCTACAGTGA 4020  
QY 4021 GTGAATTTGGAAGACTTGATGCAAAATACAAACACCAGATCCTTCTTGATTTGTTCTT 4080  
| | | | |  
Db 4021 GTGAATTTGGAAGACTTGATGCAAAATACAAACACCAGATCCTTCTTGATTTGTTCTT 4080  
QY 4081 CCAACAAATGAGGCACTAGTGTGAAGCCAGGAGTGGTCTGAGTGAACAAAGAAATGG 4140  
| | | | |  
Db 4081 CCAACAAATGAGGCACTAGTGTGAAGCCAGGAGTGGTCTGAGTGAACAAAGAAATGG 4140  
QY 4141 TTTCGATGATGAGAAAGAGAGAGGGGCTTGAAGAAATATCAAGAAAGCAAGCA 4200  
| | | | |  
Db 4141 TTTCGATGATGAGAAAGAGAGAGGGGCTTGAAGAAATATCAAGAAAGCAAGCA 4200  
QY 4201 TGGATTTCAAACTTAGTGAGAGCAGCATCTGGGTGTGAGAGTGAACAAACGCTCTGAAG 4260  
| | | | |  
Db 4201 TGGATTTCAAACTTAGTGAGAGCAGCATCTGGGTGTGAGAGTGAACAAACGCTCTGAAG 4260  
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTACATTTTAACTCAGCAGAGAGGATACCATGC 4320  
| | | | |  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTACATTTTAACTCAGCAGAGAGGATACCATGC 4320  
QY 4321 AACATTAACCTGATTAAGGCTCCAGAGAAATGGCTGAAGTGAAGCTGTGTAAGAACAG 4380  
| | | | |  
Db 4321 AACATTAACCTGATTAAGGCTCCAGAGAAATGGCTGAAGTGAAGCTGTGTAAGAACAG 4380  
QY 4381 ATGGAGGACAGGCTTCTAAGCAGCTACCTTCCATCATTAAGTACTTCTGCTTGAAG 4440  
| | | | |  
Db 4381 ATGGAGGACAGGCTTCTAAGCAGCTACCTTCCATCATTAAGTACTTCTGCTTGAAG 4440  
QY 4441 ACCTCGCGAAATCCAGAAACAGACATCGAAAAAGCAGTATTACTTACAGAAAAAGTA 4500  
| | | | |  
Db 4441 ACCTCGCGAAATCCAGAAACAGACATCGAAAAAGCAGTATTACTTACAGAAAAAGTA 4500  
QY 4501 GTGAATACCTTATAGCAGAAATCCAGAAAGGCTTCTGCTGCAAGTGTGAGAGTCTG 4560  
| | | | |  
Db 4501 GTGAATACCTTATAGCAGAAATCCAGAAAGGCTTCTGCTGCAAGTGTGAGAGTCTG 4560  
QY 4561 CAGATAGTCTTACAGTAAAAATAAAGAACAGAGTGAAGAGTCAATCCCTTCAAT 4620  
| | | | |  
Db 4561 CAGATAGTCTTACAGTAAAAATAAAGAACAGAGTGAAGAGTCAATCCCTTCAAT 4620  
QY 4621 GCCCATCTTTAGATATAGTGTGATGACATGACAGTGTGCTGAGAGTCTTCAAGATAGAA 4680  
| | | | |  
Db 4621 GCCCATCTTTAGATATAGTGTGATGACATGACAGTGTGCTGAGAGTCTTCAAGATAGAA 4680  
QY 4681 ACTACCATCTTCAAGAGAGGCTCATTAAGTGTGATGATGAGAGCAAGCTGGAG 4740  
| | | | |

Db 4681 ACTACCATCTTCAAGAGAGGCTCATTAAGTGTGATGATGAGAGCAAGCTGGAG 4740  
| | | | |  
QY 4741 ACTCTGGGCCACACGATTTGAGCGAAACATCTTACTTCCAAAGCCAGATCTAGAGGAA 4800  
| | | | |  
Db 4741 ACTCTGGGCCACACGATTTGAGCGAAACATCTTACTTCCAAAGCCAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTTCTCTGATGACCTTGAACTGTATCTTCTG 4860  
| | | | |  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTTCTCTGATGACCTTGAACTGTATCTTCTG 4860  
QY 4861 AAGACAGAGCCCCAGAGTCAAGTGTGTTGGCAACATACATCTTCAACCTCTGATTTGA 4920  
| | | | |  
Db 4861 AAGACAGAGCCCCAGAGTCAAGTGTGTTGGCAACATACATCTTCAACCTCTGATTTGA 4920  
QY 4921 AAGTTCCCAATTTGAAGTTGAGAAATCTGCCAGAGTCCAGCTGCTGCTCATCTACTG 4980  
| | | | |  
Db 4921 AAGTTCCCAATTTGAAGTTGAGAAATCTGCCAGAGTCCAGCTGCTGCTCATCTACTG 4980  
QY 4981 ATACTGCTGGGTATTAATGCAATGCAAGAAATGTGAGCAGAGGAGAAAGCCAGAAATTCAG 5040  
| | | | |  
Db 4981 ATACTGCTGGGTATTAATGCAATGCAAGAAATGTGAGCAGAGGAGAAAGCCAGAAATTCAG 5040  
QY 5041 CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTTGCTGCTGCTGCTGCTGCTGCTGCTG 5100  
| | | | |  
Db 5041 CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTTGCTGCTGCTGCTGCTGCTGCTGCTG 5100  
QY 5101 AATTTATGCTGCTGTACAAAGTTTGGCAGAAAAACACACATCATCTTAATTAATTA 5160  
| | | | |  
Db 5101 AATTTATGCTGCTGTACAAAGTTTGGCAGAAAAACACACATCATCTTAATTAATTA 5160  
QY 5161 CTGAAGAGACTCTCATGTGTGTATGAAACAGATGCTGAGTGTGTGTGTGTGTGTGTGTGTGT 5220  
| | | | |  
Db 5161 CTGAAGAGACTCTCATGTGTGTATGAAACAGATGCTGAGTGTGTGTGTGTGTGTGTGTGTGT 5220  
QY 5221 TGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGTATGCTATTTTCTGGGTGACC 5280  
| | | | |  
Db 5221 TGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGTATGCTATTTTCTGGGTGACC 5280  
QY 5281 ACTCTATTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTGG 5340  
| | | | |  
Db 5281 ACTCTATTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTGG 5340  
QY 5341 TCAATGGAAGAAACCAAGAGTCCAAAGCGAGAGAGAAATCCACAGAGAAAGATCT 5400  
| | | | |  
Db 5341 TCAATGGAAGAAACCAAGAGTCCAAAGCGAGAGAGAAATCCACAGAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTTACACACATGCCCCAGAGATCACTGG 5460  
| | | | |  
Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTTACACACATGCCCCAGAGATCACTGG 5460  
QY 5461 AATGAGTGGTACAGCTGTGTGTGCTTCTGTGTGAAGAGACCTTTCATCAATCACTCTG 5520  
| | | | |  
Db 5461 AATGAGTGGTACAGCTGTGTGTGCTTCTGTGTGAAGAGACCTTTCATCAATCACTCTG 5520  
QY 5521 GCACAGGTGTCCACCAGT 5580  
| | | | |  
Db 5521 GCACAGGTGTCCACCAGT 5580  
QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5640  
| | | | |  
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5640  
QY 5641 GTTAGCACTTACAGAGTCCAGAGAGTGCACACCTACCTGATACCCAGATCCCCACACA 5700  
| | | | |  
Db 5641 GTTAGCACTTACAGAGTCCAGAGAGTGCACACCTACCTGATACCCAGATCCCCACACA 5700  
QY 5701 GCCACTACTGA 5711  
| | | | |  
Db 5701 GCCACTACTGA 5711  
| | | | |

RESULT 10



140801 140801 5711 bp DNA PAT 01-MAY-1997  
LOCUS Sequence 10 from patent US 5622829.  
DEFINITION  
ACCESSION 140801  
NID 920822281  
KEYWORDS  
SOURCE .  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 5711)  
King, M., Friedman, L., Ostermeyer, B., Rowell, S., Lynch, E., Szabo, C.  
and Lee, M.  
TITLE Genetic markers for breast, ovarian, and prostatic cancer  
JOURNAL Patent: US 5622829-A 10 22-APR-1997;  
FEATURES Location/Qualifiers  
source 1..5711  
BASE COUNT 1956 a 1098 c 1274 g 1383 t  
ORIGIN

Query Match 99.9%; Score 5707.8; DB 6; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5709; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGCTGCTGAGACTTCTCTGCGCTTGAAGAGTACAAATGTCATTATGCTATGAGAAA 60  
Db 1 AGCTGCTGAGACTTCTCTGCGCTTGAAGAGTACAAATGTCATTATGCTATGAGAAA 60  
OY 61 COTGGCTGAGAGGCGTTCACCTCTGCTGGGTAAGTTCATTGGAACGAAAAGAA 120  
Db 61 COTGGCTGAGAGGCGTTCACCTCTGCTGGGTAAGTTCATTGGAACGAAAAGAA 120  
OY 121 TGGATTTATCTGCTCTCTGCGCTTGAAGAGTACAAATGTCATTATGCTATGAGAAA 180  
Db 121 TGGATTTATCTGCTCTCTGCGCTTGAAGAGTACAAATGTCATTATGCTATGAGAAA 180  
OY 181 TCTTGAAGTGTCCCATCTGCTGAGAGTGTATCAAGAACCTGTCTCCACAAAGTGAC 240  
Db 181 TCTTGAAGTGTCCCATCTGCTGAGAGTGTATCAAGAACCTGTCTCCACAAAGTGAC 240  
OY 241 ACATATTTTGCAATTTTGTCATGCTGAACCTCTCAACGAGAAAGGCGCTTGACACT 300  
Db 241 ACATATTTTGCAATTTTGTCATGCTGAACCTCTCAACGAGAAAGGCGCTTGACACT 300  
OY 301 GTCTTTATGTAGATGATATTAACCAAAAGAGCCTCAAGAAAGTACGAGATTAGTC 360  
Db 301 GTCTTTATGTAGATGATATTAACCAAAAGAGCCTCAAGAAAGTACGAGATTAGTC 360  
OY 361 AACTGTGTGAGAGCTATTTGAATCAATTTGTGCTTTTCAGCTTGACACAGGTTTGAGT 420  
Db 361 AACTGTGTGAGAGCTATTTGAATCAATTTGTGCTTTTCAGCTTGACACAGGTTTGAGT 420  
OY 421 ATGCAAAAGCATATTTTGAAGAAAGAAATTAACCTCTCTGAACATCTTAAAGAGT 480  
Db 421 ATGCAAAAGCATATTTTGAAGAAAGAAATTAACCTCTCTGAACATCTTAAAGAGT 480  
OY 481 AAGTTTATCATCAAAAGTATGGCTACAGAAACCGTSCCAAAAGACTTTCACAGAGT 540  
Db 481 AAGTTTATCATCAAAAGTATGGCTACAGAAACCGTSCCAAAAGACTTTCACAGAGT 540  
OY 541 AACCCGAAATATCTTCTTGTGACGAAACAGTCTCAAGTCTCTTAACCTTTGGA 600  
Db 541 AACCCGAAATATCTTCTTGTGACGAAACAGTCTCAAGTCTCTTAACCTTTGGA 600  
OY 601 CTGTGAGAACTGTGAGCAAGGAGATCAACCTCAAAAGAGCTGTGCTACATTG 660  
Db 601 CTGTGAGAACTGTGAGCAAGGAGATCAACCTCAAAAGAGCTGTGCTACATTG 660  
OY 661 AATTGGAGTCTATTTCTCTGAGATACCGTTAATTAAGCAACTTATTTGAGTGGAG 720  
Db 661 AATTGGAGTCTATTTCTCTGAGATACCGTTAATTAAGCAACTTATTTGAGTGGAG 720

OY 721 ATCAAGATTTGTTACAAATCAACCCCTCAAGGACGAGGATGAATCACTTTGATCTG 780  
Db 721 ATCAAGATTTGTTACAAATCAACCCCTCAAGGACGAGGATGAATCACTTTGATCTG 780  
OY 781 CAAAAAGGCTCTGTGTAATTTTCTGAGAGCGATGTAACTAATCTAATCATCTAAC 840  
Db 781 CAAAAAGGCTCTGTGTAATTTTCTGAGAGCGATGTAACTAATCTAATCATCTAAC 840  
OY 841 CCAGTAAATATGATTTGAACACACACTGAGAAAGCGTGCAGCTGAGAGCATCCAGAAAGT 900  
Db 841 CCAGTAAATATGATTTGAACACACACTGAGAAAGCGTGCAGCTGAGAGCATCCAGAAAGT 900  
OY 901 ATCAGAGTATGTTCTTTTCAAACTGCAATGTGAGACCATGTGCGCAAAATATCTATGCCA 960  
Db 901 ATCAGAGTATGTTCTTTTCAAACTGCAATGTGAGACCATGTGCGCAAAATATCTATGCCA 960  
OY 961 GCTATTACAGCATGAGAACAGCATTTATTTACTACATTAAGACAGAAATGATGAGAAA 1020  
Db 961 GCTATTACAGCATGAGAACAGCATTTATTTACTACATTAAGACAGAAATGATGAGAAA 1020  
OY 1021 AGGCTGAATTTCTGTATATAAAACCAACAGCCCTGCTTAGCAAGAGCCAACTAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTATATAAAACCAACAGCCCTGCTTAGCAAGAGCCAACTAACAGAT 1080  
OY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACCTCCAGCACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACCTCCAGCACAGAAAAAGGTAG 1140  
OY 1141 ATCTGAATGCTGATCCCTGCTGAGAGAAAGATGGAATTAAGCAGAAACCTGCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGCTGAGAGAAAGATGGAATTAAGCAGAAACCTGCATGCT 1200  
OY 1201 CAGAGAAATCTAGAGATCTGAAGATGTTCTTGTGATACACTAAATAGACATTCAGA 1260  
Db 1201 CAGAGAAATCTAGAGATCTGAAGATGTTCTTGTGATACACTAAATAGACATTCAGA 1260  
OY 1261 AAGTTAATGAGTGTGTTTCCAGAAATGATGAACCTGTATAGTTCTATGACTACATGATG 1320  
Db 1261 AAGTTAATGAGTGTGTTTCCAGAAATGATGAACCTGTATAGTTCTATGACTACATGATG 1320  
OY 1321 GGGAGTCTGAATCAAAATGCCAAAGAGCTGATGTATGAGAGCTTGAATGAGTATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGAGCTGATGTATGAGAGCTTGAATGAGTATG 1380  
OY 1381 AATATTCTGTTCTTCAAGAGAAATAGACTTACTGGCCAGTGTATCTATGAGGCTTTAA 1440  
Db 1381 AATATTCTGTTCTTCAAGAGAAATAGACTTACTGGCCAGTGTATCTATGAGGCTTTAA 1440  
OY 1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAATGATGAGAGTAAATTTAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAATGATGAGAGTAAATTTAAGCAAAATAT 1500  
OY 1501 TTGGGAAAAACGTATGGAAGAAAGGCAAGCCTCCCACTTAAGCCATGAATCTGAAATC 1560  
Db 1501 TTGGGAAAAACGTATGGAAGAAAGGCAAGCCTCCCACTTAAGCCATGAATCTGAAATC 1560  
OY 1561 TAATATAGAGACATTTTACTAGGACAGAGATTAATCAAGAGCGTCCCTCACAATA 1620  
Db 1561 TAATATAGAGACATTTTACTAGGACAGAGATTAATCAAGAGCGTCCCTCACAATA 1620  
OY 1621 AATTAAAGCGTAAAGAGACCTACATAGGCTTCATCTGAGAGATTTTAAACAAGAAAG 1680  
Db 1621 AATTAAAGCGTAAAGAGACCTACATAGGCTTCATCTGAGAGATTTTAAACAAGAAAG 1680  
OY 1681 CAGATTTGGAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTAACCAAGAGAGC 1740  
Db 1681 CAGATTTGGAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTAACCAAGAGAGC 1740  
OY 1741 AGAATGCTCAAGTGAATGATTTTAAATAGTGTGATGATGATTAATTAAGTGTGAT 1800  
Db 1741 AGAATGCTCAAGTGAATGATTTTAAATAGTGTGATGATGATTAATTAAGTGTGAT 1800  
OY 1801 CTATTCAAGATGAGAAAAATCTTAACCAATTAAGATCACTCGAAAAAGATCTGCTTCA 1860

```
Db 1801 CTTATTCGAATGAGAAAAATCCTTAACCCATAGAAATCACTCGAAAAAGAAATCTGTTTCA 1860
Qy 1861 AAMGAAAGCTGAACCTTAAGACAGACAGTATAGCAATATGAGACTCGAATTAATATCC 1920
Db 1861 AAMGAAAGCTGAACCTTAAGACAGACAGTATAGCAATATGAGACTCGAATTAATATCC 1920
Qy 1921 ACAATTTCAAAAGCACCTTAAAAAGATAGGCTGAGAGAGAGAGTCTTCTACACGACATATTC 1980
Db 1921 ACAATTTCAAAAGCACCTTAAAAAGATAGGCTGAGAGAGAGAGTCTTCTACACGACATATTC 1980
Qy 1981 ATGGCTTGAAGTACTAGTACTGATAGAAATCTAAGCCCACTTAATGTGTGTAATGCAAA 2040
Db 1981 ATGGCTTGAAGTACTAGTACTGATAGAAATCTAAGCCCACTTAATGTGTGTAATGCAAA 2040
Qy 2041 TTGATAGTGTCTTAGCAGTAGAGATAGAGAAAAAAGATACAAACCAATGGCCAGTCA 2100
Db 2041 TTGATAGTGTCTTAGCAGTAGAGATAGAGAAAAAAGATACAAACCAATGGCCAGTCA 2100
Qy 2101 GGCACACAGAAACCTTACACTCATGGAAGGTAAAAAAGCTGCAACTGGAGCCAAAGAA 2160
Db 2101 GGCACACAGAAACCTTACACTCATGGAAGGTAAAAAAGCTGCAACTGGAGCCAAAGAA 2160
Qy 2161 GTAACAAGCCAAATGAAAGACAGCAAGTAAAGACATGACAGGATCTTCCAGAGCTGA 2220
Db 2161 GTAACAAGCCAAATGAAAGACAGCAAGTAAAGACATGACAGGATCTTCCAGAGCTGA 2220
Qy 2221 AGTTAACAAATGCACTGGTCTTTTACTAAGTGTTCAAATACAGAGTAAAGAT 2280
Db 2221 AGTTAACAAATGCACTGGTCTTTTACTAAGTGTTCAAATACAGAGTAAAGAT 2280
Qy 2281 TTGTCAATCTAGGCTTCCAGAGAGAAAAAAGAGAAACCTAGAAACAGTTAAAGTGT 2340
Db 2281 TTGTCAATCTAGGCTTCCAGAGAGAAAAAAGAGAAACCTAGAAACAGTTAAAGTGT 2340
Qy 2341 CTATATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACTG 2400
Db 2341 CTATATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACTG 2400
Qy 2401 AAGATCTGTAGAGATGACAGATATTCATTGTAACCTGGTACGATTAATGGCACTAGG 2460
Db 2401 AAGATCTGTAGAGATGACAGATATTCATTGTAACCTGGTACGATTAATGGCACTAGG 2460
Qy 2461 AAGTATCTGTTACTGAGAGTATGCACTCTAGGGAAGGCAAAAAACAAATTAAT 2520
Db 2461 AAGTATCTGTTACTGAGAGTATGCACTCTAGGGAAGGCAAAAAACAAATTAAT 2520
Qy 2521 GTGTGAGTCAAGTGTGACGATTTTGAAGAACCCCAAGGCACTAATTCATGTTGCCAAG 2580
Db 2521 GTGTGAGTCAAGTGTGACGATTTTGAAGAACCCCAAGGCACTAATTCATGTTGCCAAG 2580
Qy 2581 ATATATGAAAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAATTAACCAAGTC 2640
Db 2581 ATATATGAAAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAATTAACCAAGTC 2640
Qy 2641 GGGAAACAACCATAGAAATGGAAGAAAGTGAATCTGATGCTCAATATTGGAGATACAT 2700
Db 2641 GGGAAACAACCATAGAAATGGAAGAAAGTGAATCTGATGCTCAATATTGGAGATACAT 2700
Qy 2701 TCAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAAAATCCAGGAATGCAAGAAAGG 2760
Db 2701 TCAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAAAATCCAGGAATGCAAGAAAGG 2760
Qy 2761 AATGTGCAACATTTCTGTCCCACTGTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820
Db 2761 AATGTGCAACATTTCTGTCCCACTGTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820
Qy 2821 TTGAATGTGAACAAAGGAAGAAATTAAGGAAAGATGAGTCTAATATCAAGCTGTAC 2880
Db 2821 TTGAATGTGAACAAAGGAAGAAATTAAGGAAAGATGAGTCTAATATCAAGCTGTAC 2880
Qy 2881 AGACAGTATATATCACTGACGAGCTTCTGTGTTGTCAGAAAGATTAAGCAAGTTGATA 2940
Db 2881 AGACAGTATATATCACTGACGAGCTTCTGTGTTGTCAGAAAGATTAAGCAAGTTGATA 2940

Db 2881 AGACAGTATATATCACTGACGAGCTTCTGTGTTGTCAGAAAGATTAAGCAAGTTGATA 2940
Qy 2941 ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCACTGAGAGCA 3000
Db 2941 ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCACTGAGAGCA 3000
Qy 3001 ACGAAATGGAAGTCAATCTCCAAATTAACATGAGACTTTTACAAAACCCATATCTATAC 3060
Db 3001 ACGAAATGGAAGTCAATCTCCAAATTAACATGAGACTTTTACAAAACCCATATCTATAC 3060
Qy 3061 CACCACTTTTCCCATCAAGTCAATGTTTAAACTTAATAGAAAAAATCTCTAGAG 3120
Db 3061 CACCACTTTTCCCATCAAGTCAATGTTTAAACTTAATAGAAAAAATCTCTAGAG 3120
Qy 3121 AAAACTTTGAGGAACATTCATCTCACCTGAAGAGAAATGAGAAATGAGACATTCGAA 3180
Db 3121 AAAACTTTGAGGAACATTCATCTCACCTGAAGAGAAATGAGAAATGAGACATTCGAA 3180
Qy 3181 GTACAGTGAAGCAATTAAGCCGTAAATACATTAAGAAAAATGTTTAAAGAACCAAGCT 3240
Db 3181 GTACAGTGAAGCAATTAAGCCGTAAATACATTAAGAAAAATGTTTAAAGAACCAAGCT 3240
Qy 3241 CAAGCAATATTAATGAAGTATAGTTCAGTACTATGAAGTGGGCTCCAGTATTAATGAA 3300
Db 3241 CAAGCAATATTAATGAAGTATAGTTCAGTACTATGAAGTGGGCTCCAGTATTAATGAA 3300
Qy 3301 TAGGTTCCAGTATGAAGAAATTCACAGACAGACTAGTAGAAACAGAGGCAAAATTTGA 3360
Db 3301 TAGGTTCCAGTATGAAGAAATTCACAGACAGACTAGTAGAAACAGAGGCAAAATTTGA 3360
Qy 3361 ATGCTATGCTTAGATTAAGGGGTTTGGCACTGAGGCTCTAATAACAAAGTCTCTGAA 3420
Db 3361 ATGCTATGCTTAGATTAAGGGGTTTGGCACTGAGGCTCTAATAACAAAGTCTCTGAA 3420
Qy 3421 GTAATGTGAAGCAATCCGAAATTAAGAAAGAAATATGAAGATGACAGTCTGTA 3480
Db 3421 GTAATGTGAAGCAATCCGAAATTAAGAAAGAAATATGAAGATGACAGTCTGTA 3480
Qy 3481 ATACAGATTTCTCTCATCTATCTGATTTCAAGTAACTTAGAACAGCTTAATGGGAAGTAC 3540
Db 3481 ATACAGATTTCTCTCATCTATCTGATTTCAAGTAACTTAGAACAGCTTAATGGGAAGTAC 3540
Qy 3541 ATGCTATCTCAGGTTTGTCTGACACACCTGATGACCTGTTAGTATGTAATTAAG 3600
Db 3541 ATGCTATCTCAGGTTTGTCTGACACACCTGATGACCTGTTAGTATGTAATTAAG 3600
Qy 3601 AAGTACTAGTTTGGCAAAATGACATTAAGAAAGTCTGCTGTTTACCAAAAGG 3660
Db 3601 AAGTACTAGTTTGGCAAAATGACATTAAGAAAGTCTGCTGTTTACCAAAAGG 3660
Qy 3661 TCCGAAAGGAGAGCTTAGCAGAGTCTAGCCCTTTCACCCATACATATTTGGCTCAGG 3720
Db 3661 TCCGAAAGGAGAGCTTAGCAGAGTCTAGCCCTTTCACCCATACATATTTGGCTCAGG 3720
Qy 3721 GTTACGGAAGAGGGGCCAAGAAATTAAGTCTCAGAAAGAACTTATCTAGAGGATG 3780
Db 3721 GTTACGGAAGAGGGGCCAAGAAATTAAGTCTCAGAAAGAACTTATCTAGAGGATG 3780
Qy 3781 AAGAGCTTCCCTGCTCCAAACTGTTAATGTGTAATTAACATATTAACCTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTCCAAACTGTTAATGTGTAATTAACATATTAACCTCTCAGT 3840
Qy 3841 CTACTAGGCAATGACACGCTGTGACAGATGCTGTCTAAGAAACAGAGAGAAATTTAT 3900
Db 3841 CTACTAGGCAATGACACGCTGTGACAGATGCTGTCTAAGAAACAGAGAGAAATTTAT 3900
Qy 3901 TATCATTTGAAGAAATAGCTTAATAGTCAAGTACCAAGGTAATTTGGCAAGGATCTC 3960
Db 3901 TATCATTTGAAGAAATAGCTTAATAGTCAAGTACCAAGGTAATTTGGCAAGGATCTC 3960
Qy 3961 AGGACATCACTTATGAGGAAACAAATATGTTGCTAGCTTGTCTTCTACAGTGCA 4020
Db 3961 AGGACATCACTTATGAGGAAACAAATATGTTGCTAGCTTGTCTTCTTCTACAGTGCA 4020
```

QY 4021 GTGAATGGAGACTTGATCGCAATACAAACCCAGATCCTTTCTGATTGGTCTT 4080  
 DB 4021 GTGAATGGAGACTTGATCGCAATACAAACCCAGATCCTTTCTGATTGGTCTT 4080  
 QY 4081 CCAACAAATGAGGCGATCGTGAAGGCGAGGAGTGGTCTGAGTGAAGGAATGG 4140  
 DB 4081 CCAACAAATGAGGCGATCGTGAAGGCGAGGAGTGGTCTGAGTGAAGGAATGG 4140  
 QY 4141 TTTCAGATGATGAGAAAGAGAAAGGCGCTTGGAAAGAAATATCAAGAAAGCAAGCA 4200  
 DB 4141 TTTCAGATGATGAGAAAGAGAAAGGCGCTTGGAAAGAAATATCAAGAAAGCAAGCA 4200  
 QY 4201 TGGATCAAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAAGCAAGCGTCTGAAG 4260  
 DB 4201 TGGATCAAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAAGCAAGCGTCTGAAG 4260  
 QY 4261 ACTGCTCAGGCGATCCTCTCAGAGTACATTTTACCACTGACGAGAGGATACCATGC 4320  
 DB 4261 ACTGCTCAGGCGATCCTCTCAGAGTACATTTTACCACTGACGAGAGGATACCATGC 4320  
 QY 4321 AACATACCTGATTAAGCTCCAGCAGAAATGGCTGAAGTGTGTTGAACAGC 4380  
 DB 4321 AACATACCTGATTAAGCTCCAGCAGAAATGGCTGAAGTGTGTTGAACAGC 4380  
 QY 4381 ATGGAGCCAGCCTTAAACAGCTACCTTCCATTAAGTGAAGTCTTCTGCCCTTGAGG 4440  
 DB 4381 ATGGAGCCAGCCTTAAACAGCTACCTTCCATTAAGTGAAGTCTTCTGCCCTTGAGG 4440  
 QY 4441 ACCTGCAATCCAGAAACAGCATCAAGAAAGCAATTAATCTTACAGAAAGTA 4500  
 DB 4441 ACCTGCAATCCAGAAACAGCATCAAGAAAGCAATTAATCTTACAGAAAGTA 4500  
 QY 4501 GTGAATACCTTAATTAAGCCAGAAATCCAGAAAGCCTTCTGCTGCAAGTGTGAGTCTG 4560  
 DB 4501 GTGAATACCTTAATTAAGCCAGAAATCCAGAAAGCCTTCTGCTGCAAGTGTGAGTCTG 4560  
 QY 4561 CAGATAGTCTACAGTAAATTAAGAAACAGAGTGAAGAGTATCCCTTCTTAAT 4620  
 DB 4561 CAGATAGTCTACAGTAAATTAAGAAACAGAGTGAAGAGTATCCCTTCTTAAT 4620  
 QY 4621 GCCCATCATTAATGATAGTGTGATACATCAGAGTGTCTGGAGTCTTCAAGAAATGAA 4680  
 DB 4621 GCCCATCATTAATGATAGTGTGATACATCAGAGTGTCTGGAGTCTTCAAGAAATGAA 4680  
 QY 4681 ACTACCATCTCAGAGAGCTCATTAAGTGTGATGATGAGAGCAACAGCTGGAAG 4740  
 DB 4681 ACTACCATCTCAGAGAGCTCATTAAGTGTGATGATGAGAGCAACAGCTGGAAG 4740  
 QY 4741 AGTCTGGGCGCAGATTTGAGGAAACATCTTACTTGCAGAGCAAGATCTAGAGGAA 4800  
 DB 4741 AGTCTGGGCGCAGATTTGAGGAAACATCTTACTTGCAGAGCAAGATCTAGAGGAA 4800  
 QY 4801 CCCCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4860  
 DB 4801 CCCCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4860  
 QY 4861 AAGACAGAGCCCGAGAGTACGCTGTTGGCAATACCATCTTCAACCTGCAATGA 4920  
 DB 4861 AAGACAGAGCCCGAGAGTACGCTGTTGGCAATACCATCTTCAACCTGCAATGA 4920  
 QY 4921 AAGTCTCCCAATTTGAAGTTCAGAAATCTGCCAGAGTCCAGCTGCTCATACTAGT 4980  
 DB 4921 AAGTCTCCCAATTTGAAGTTCAGAAATCTGCCAGAGTCCAGCTGCTCATACTAGT 4980  
 QY 4981 ATACTGCTGGATTAATGCAATGGAAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040  
 DB 4981 ATACTGCTGGATTAATGCAATGGAAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040  
 QY 5041 CTTCACAGAGAGGCTCAACAAAGATGTCATGTTGTTGCTGCTGACCCGAGAG 5100  
 DB 5041 CTTCACAGAGAGGCTCAACAAAGATGTCATGTTGTTGCTGCTGACCCGAGAG 5100

QY 5101 AATTTATGCTGCTGACAAAGTTGGCAGAAACACCACATCACTTTACTAATTA 5160  
 DB 5101 AATTTATGCTGCTGACAAAGTTGGCAGAAACACCACATCACTTTACTAATTA 5160  
 QY 5161 CTGAAGAGACTACATGTTGTTATGAAAGAGATGCTGAGTGTGAGAGGAGAC 5220  
 DB 5161 CTGAAGAGACTACATGTTGTTATGAAAGAGATGCTGAGTGTGAGAGGAGAC 5220  
 QY 5221 TGAATATTTTCTAGAAATGGGAGGAGAAATGGGATGATTAATTTCTGGGTACCC 5280  
 DB 5221 TGAATATTTTCTAGAAATGGGAGGAGAAATGGGATGATTAATTTCTGGGTACCC 5280  
 QY 5281 AGCTATTAAAGAAAGAAATGCTGATGACATGATTTTGAAGTCAAGAGATGTGG 5340  
 DB 5281 AGCTATTAAAGAAAGAAATGCTGATGACATGATTTTGAAGTCAAGAGATGTGG 5340  
 QY 5341 TCAATGGAAGAAACCAAGGTCCTCAAGGCGAGCAAGAAATCCAGAGCAGAAAGATCT 5400  
 DB 5341 TCAATGGAAGAAACCAAGGTCCTCAAGGCGAGCAAGAAATCCAGAGCAGAAAGATCT 5400  
 QY 5401 TCAGGGGGCTAGAAATCTGTTCTATGAGGCGCTTCAACCAATGCCCACAGATCACTGG 5460  
 DB 5401 TCAGGGGGCTAGAAATCTGTTCTATGAGGCGCTTCAACCAATGCCCACAGATCACTGG 5460  
 QY 5461 AATGATGCTACAGCTGTGTGCTTCTGTGTGTAAGAGCTTTTCAATTCACCTTG 5520  
 DB 5461 AATGATGCTACAGCTGTGTGCTTCTGTGTGTAAGAGCTTTTCAATTCACCTTG 5520  
 QY 5521 GCACAGGCTGCCACCAATGTTGTTGTCAGCAGATGCTGAGAGAGCAATGGCT 5580  
 DB 5521 GCACAGGCTGCCACCAATGTTGTTGTCAGCAGATGCTGAGAGAGCAATGGCT 5580  
 QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGTGTGGACA 5640  
 DB 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGTGTGGACA 5640  
 QY 5641 GTGTAGCTACTTACCAAGTGTGAGGAGCTGTGTGTGACCCGAGAGTGGTGTGGACA 5700  
 DB 5641 GTGTAGCTACTTACCAAGTGTGAGGAGCTGTGTGTGACCCGAGAGTGGTGTGGACA 5700  
 QY 5701 GGCCTACTGA 5711  
 DB 5701 GGCCTACTGA 5711

RESULT 11  
 AR007335  
 LOCUS AR007335 5711 bp DNA PAT 04-DEC-1998  
 DEFINITION Sequence 5 from patent US 5750400.  
 ACCESSION AR007335  
 KEYWORDS 93966819  
 NID  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 UNKNOWN.  
 REFERENCE 1 (bases 1 to 5711)  
 MURPHY, P.D., ALLEN, A.C., ALVARES, C.P., CRITZ, B.S., OLSON, S.J.,  
 SCHLEIFER, D.B. and ZENG, B.  
 TITLE Coding sequences of the human BRCA1 gene  
 JOURNAL Patent: US 5750400-A 5 12-MAY-1998;  
 FEATURES  
 source  
 1. 5711  
 BASE COUNT 1953 a 1098 c 1277 g 1383 t  
 ORIGIN

Query Match 99.9%; Score 5703; DB 6; Length 5711;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 ACCTGCTGAGACTCTGAGACCCGACACAGCTGTGGGCTTCTCAGATTAAGTGGCC 60

Db 1 AGCTCGTAGACTTCCTGGAGCCCGCACAGGCTGTGGGGTTTCTCAAGTAACAGTGGCC 60  
Qy 61 CCTGGCTCAGAGAGGCTTCCACCTCTGCTGGTAAAGTTTCATTTGGAACAGAAAGAA 120  
Db 61 CCTGGCTCAGAGAGGCTTCCACCTCTGCTGGTAAAGTTTCATTTGGAACAGAAAGAA 120  
Qy 121 TGGATTTATCTCTCTCTCGCGTTGAAGAAATGTCATTAATGCTATGCAAGAAA 180  
Db 121 TGGATTTATCTCTCTCTCGCGTTGAAGAAATGTCATTAATGCTATGCAAGAAA 180  
Qy 181 TCTTAGAGTCCCATCTCTGTGAGTTGATCAAGAGACCTGTCTCCACAAAGTGTACC 240  
Db 181 TCTTAGAGTCCCATCTCTGTGAGTTGATCAAGAGACCTGTCTCCACAAAGTGTACC 240  
Qy 241 ACATATTTTGCAAATTTTGCATGCTGAAACCTTCTCAACGAGAAAGAGGCTTCACAGT 300  
Db 241 ACATATTTTGCAAATTTTGCATGCTGAAACCTTCTCAACGAGAAAGAGGCTTCACAGT 300  
Qy 301 GTCCCTTATGTAAGATGATATACCAAAAGAGCTTACAAAGAAATAGAGATTTAGTC 360  
Db 301 GTCCCTTATGTAAGATGATATACCAAAAGAGCTTACAAAGAAATAGAGATTTAGTC 360  
Qy 361 AACTGTGTAAGAGCTATGTAAGAAATCATTTGTCTTTCAGTTGACACAGGTTTGAAGT 420  
Db 361 AACTGTGTAAGAGCTATGTAAGAAATCATTTGTCTTTCAGTTGACACAGGTTTGAAGT 420  
Qy 421 ATGCAACAGCTATTAATTTTGCAGAAAAGAAAATTAATCTCTCTGTAACATCTTAAAGATG 480  
Db 421 ATGCAACAGCTATTAATTTTGCAGAAAAGAAAATTAATCTCTCTGTAACATCTTAAAGATG 480  
Qy 481 AAGTTTCTATCTCCAAAGATAGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCTCCAAAGATAGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
Qy 541 AACCCGAAATCTCTCTCTGAGAAAACAGCTCAGTCCCACTCTTAACTTGGAA 600  
Db 541 AACCCGAAATCTCTCTCTGAGAAAACAGCTCAGTCCCACTCTTAACTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATACAACTCAAAAAGAGCTCTGTCTACATTG 660  
Db 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATACAACTCAAAAAGAGCTCTGTCTACATTG 660  
Qy 661 AATGGAGATCTGATCTCTGTAAGATACCGTTAATTAAGCAACTTCTGACAGTGGGAG 720  
Db 661 AATGGAGATCTGATCTCTGTAAGATACCGTTAATTAAGCAACTTCTGACAGTGGGAG 720  
Qy 721 ATCAAGATTTGTTACAAATCAACCCCTCAAGGAACAGGATGAATCAGTTTGGATTCTG 780  
Db 721 ATCAAGATTTGTTACAAATCAACCCCTCAAGGAACAGGATGAATCAGTTTGGATTCTG 780  
Qy 781 CAAAAAGGCTGCTGTGAATTTTCTGAGAGGATGTAACAAAATACATCATCAAC 840  
Db 781 CAAAAAGGCTGCTGTGAATTTTCTGAGAGGATGTAACAAAATACATCATCAAC 840  
Qy 841 CCAGTAATTAATGATTTGAACACCACTGAGAGAGCTGACAGGCAATCCAGAAAT 900  
Db 841 CCAGTAATTAATGATTTGAACACCACTGAGAGAGCTGACAGGCAATCCAGAAAT 900  
Qy 901 ATCAGAGTGTCTGTTTCAAACTGATGTGAGGCTGTGGCACAATTAAGTACATGCA 960  
Db 901 ATCAGAGTGTCTGTTTCAAACTGATGTGAGGCTGTGGCACAATTAAGTACATGCA 960  
Qy 961 GCTCATTTACAGATGAGAACAGAGTTTATTAATCTCACTAAGAGCAAGAAATGATGAAA 1020  
Db 961 GCTCATTTACAGATGAGAACAGAGTTTATTAATCTCACTAAGAGCAAGAAATGATGAAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATAAAGCAAAAGCCTGGCTTACCAAGAGGCAACATTAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATAAAGCAAAAGCCTGGCTTACCAAGAGGCAACATTAACAGAT 1080  
Qy 1081 GGGCTGAAGTAAAGAAACATGTAATGATAGGCGAGCTCCAGCAGAGAAAAGAGTAA 1140  
Db 1081 GGGCTGAAGTAAAGAAACATGTAATGATAGGCGAGCTCCAGCAGAGAAAAGAGTAA 1140

Qy 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGGAATTAACAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGGAATTAACAGAACTGCCATGCT 1200  
Qy 1201 CAGAGAAATCTGAGATACTGAAGATGTTTCTGGATTAACCTAATAATAGCAGATTGAGA 1260  
Db 1201 CAGAGAAATCTGAGATACTGAAGATGTTTCTGGATTAACCTAATAATAGCAGATTGAGA 1260  
Qy 1261 AAGTTAATAGTGTGTTTCCAGAAAGTGAATGAACTGTAGTTCTGATGACTCAATGATG 1320  
Db 1261 AAGTTAATAGTGTGTTTCCAGAAAGTGAATGAACTGTAGTTCTGATGACTCAATGATG 1320  
Qy 1321 GGGAGTCTGAATCAATATGCCAAAGTACTGATGTAATTTGGACGTTCTAATAGGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAATATGCCAAAGTACTGATGTAATTTGGACGTTCTAATAGGTAGATG 1380  
Qy 1381 AATATTTGCTTCTCAGAGAAATAGAACTTACAGGAGATCCATGAGGCTTAA 1440  
Db 1381 AATATTTGCTTCTCAGAGAAATAGAACTTACAGGAGATCCATGAGGCTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTCACCTCAATCAGTAGAGTAATATTGAGAACAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTCACCTCAATCAGTAGAGTAATATTGAGAACAAATAT 1500  
Qy 1501 TTGGGAAAACCTATCGGAAGAAAGCAGCCCTCCCACTTAAGCATGTAATGAAAATC 1560  
Db 1501 TTGGGAAAACCTATCGGAAGAAAGCAGCCCTCCCACTTAAGCATGTAATGAAAATC 1560  
Qy 1561 TAATTTATGAGCAATTTTCTTCTGAGCCAGATTAATTAACAGAGCGTCCCTCAATA 1620  
Db 1561 TAATTTATGAGCAATTTTCTTCTGAGCCAGATTAATTAACAGAGCGTCCCTCAATA 1620  
Qy 1621 AATTAAGCGTAAAGAGAGACTACATCAGGCTTCACTCAGAGATTTATCAAGAAAG 1680  
Db 1621 AATTAAGCGTAAAGAGAGACTACATCAGGCTTCACTCAGAGATTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAATGATTAATCAGGAACTTACCAAGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAATGATTAATCAGGAACTTACCAAGGAGC 1740  
Qy 1741 AGAATGTCAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800  
Db 1741 AGAATGTCAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800  
Qy 1801 CTATTCAGAAATGAGAAATATCTTAACCAATAGATCACTCGAAGAAAGAAATCTGCTTCA 1860  
Db 1801 CTATTCAGAAATGAGAAATATCTTAACCAATAGATCACTCGAAGAAAGAAATCTGCTTCA 1860  
Qy 1861 AAAGCAAGCTGAACTTAATTAAGCAGAGTATTAAGCAATATGAACTGAAATTAATTC 1920  
Db 1861 AAAGCAAGCTGAACTTAATTAAGCAGAGTATTAAGCAATATGAACTGAAATTAATTC 1920  
Qy 1921 ACAATTTCAAAAGCACTTAAAGAAATAGCTGAGAGGAAATCTTCTCAAGAGATATTC 1980  
Db 1921 ACAATTTCAAAAGCACTTAAAGAAATAGCTGAGAGGAAATCTTCTCAAGAGATATTC 1980  
Qy 1981 ATGCGCTGAAGTACTAGTATGAAATCTTAAGCCCACTTAATTTAGTAAATGCAAA 2040  
Db 1981 ATGCGCTGAAGTACTAGTATGAAATCTTAAGCCCACTTAATTTAGTAAATGCAAA 2040  
Qy 2041 TTGATAGTGTCTTACAGTAGAGATTAAGAAAAAAGTATACAAACCAATATGCAATGCA 2100  
Db 2041 TTGATAGTGTCTTACAGTAGAGATTAAGAAAAAAGTATACAAACCAATATGCAATGCA 2100  
Qy 2101 GGCACAGCAAGAACTTAACATCTGAGAGGTAAGAACTGCAACTGCAAGTGAAGAGAA 2160  
Db 2101 GGCACAGCAAGAACTTAACATCTGAGAGGTAAGAACTGCAACTGCAAGTGAAGAGAA 2160  
Qy 2161 GTAAACAGCCAAATGAAGACAGCAAGTAAAGACATGACAGAGATCTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAAGACAGCAAGTAAAGACATGACAGAGATCTTCCAGAGCTGA 2220

Qy	2221	AGTTAAACAATGCACCCGTGGTCTCTTTACTPAAGGTCCAATACCACTGAACCTTAAGAT	2280
Db	2221	AGTTAAACAATGCACCCGTGGTCTCTTTACTPAAGGTCCAATACCACTGAACCTTAAGAT	2280
Qy	2281	TTGTCAATCCTAGCCTTCCAAAGAAAGAAAAGAAAGAAATCAGAAAAGTTAAAGCT	2340
Db	2281	TTGTCAATCCTAGCCTTCCAAAGAAAGAAAAGAAAGAAATCAGAAAAGTTAAAGCT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGAGTCATGTTAAGTGGAGAAAGGGTTTTCAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGAGTCATGTTAAGTGGAGAAAGGGTTTTCAACTG	2400
Qy	2401	AAATATCTGTAGAGAGTAGACATATTTTCATGGTACTGCTGTCTGATTATGGCACTAG	2460
Db	2401	AAATATCTGTAGAGAGTAGACATATTTTCATGGTACTGCTGTCTGATTATGGCACTAG	2460
Qy	2461	AAATATCTGTAGAGAGTAGACATATTTTCATGGTACTGCTGTCTGATTATGGCACTAG	2520
Db	2461	AAATATCTGTAGAGAGTAGACATATTTTCATGGTACTGCTGTCTGATTATGGCACTAG	2520
Qy	2521	GTTGTAGTCAGTGTGCAGCATTTTGAAGACCCCAAGGAGCTAATTCATGGTGTTCCAAG	2580
Db	2521	GTTGTAGTCAGTGTGCAGCATTTTGAAGACCCCAAGGAGCTAATTCATGGTGTTCCAAG	2580
Qy	2581	ATTAATAAAATGACACAGAAGCCTTTAAGTATCATGTGGACATAGATTAAACACAGTC	2640
Db	2581	ATTAATAAAATGACACAGAAGCCTTTAAGTATCATGTGGACATAGATTAAACACAGTC	2640
Qy	2641	GGGAAACAAGCATAGAAATGGAGAAAGTAAGTAAGTCACTAGTATTTGCGAATATAT	2700
Db	2641	GGGAAACAAGCATAGAAATGGAGAAAGTAAGTAAGTCACTAGTATTTGCGAATATAT	2700
Qy	2701	TCAAGTTTCAAGCGCCAGTCATTTTGTCTGTCTTTCCAATCCAGGAAATGCAGAGAG	2760
Db	2701	TCAAGTTTCAAGCGCCAGTCATTTTGTCTGTCTTTCCAATCCAGGAAATGCAGAGAG	2760
Qy	2761	AAITGCAACATTTCTGTGCCACTGTGGCTCTTAAGAACAAGTCCAAAAGTCACTT	2820
Db	2761	AAITGCAACATTTCTGTGCCACTGTGGCTCTTAAGAACAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGTAAGTCTAATATCAAGCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGTAAGTCTAATATCAAGCCTGTAC	2880
Qy	2881	AGACAGTTAATATCAGTCAGCGCTTCTGTGTGGTGTGTCAGAAAGATAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCAGTCAGCGCTTCTGTGTGGTGTGTCAGAAAGATAGCCAGTTGATA	2940
Qy	2941	ATGCCAAATGTAGTATCAAGAGAGCCTCTAAGTTTGTCTATCATCTCAGTTCAGAGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAGAGAGCCTCTAAGTTTGTCTATCATCTCAGTTCAGAGCA	3000
Qy	3001	ACGAAACTGACATCTTACCTCCAAATTAACATGAGATCTTAAACCAATATGCTATAC	3060
Db	3001	ACGAAACTGACATCTTACCTCCAAATTAACATGAGATCTTAAACCAATATGCTATAC	3060
Qy	3061	CACACATTTTCCCATCAATGATCTTTGTTAAACTTAATGTAGAAAAATCTGCTAGAGG	3120
Db	3061	CACACATTTTCCCATCAATGATCTTTGTTAAACTTAATGTAGAAAAATCTGCTAGAGG	3120
Qy	3121	AAAACTTGAAGAACATTCATGTCACTGCAAGAGAAATGGGAAATGAGAACATTCGA	3180
Db	3121	AAAACTTGAAGAACATTCATGTCACTGCAAGAGAAATGGGAAATGAGAACATTCGA	3180
Qy	3181	GTCAGTGACACAAATTAGCCGTAAATTAACATTTAGAAAAATGTTTAAAGAGCCAGCT	3240
Db	3181	GTCAGTGACACAAATTAGCCGTAAATTAACATTTAGAAAAATGTTTAAAGAGCCAGCT	3240
Qy	3241	CAACCAATTTAAATGAAGTGTGTTCCAGTACATTAAGATGAGGCTCCAGTATTAATGAA	3300
Db	3241	CAACCAATTTAAATGAAGTGTGTTCCAGTACATTAAGATGAGGCTCCAGTATTAATGAA	3300
Qy	3301	TAGGTTCCAGTATGAAGAACATTCAGCAGAACATAGTGGAAACAGAGGCCAAATATGA	3360

Db	3301	TAGGTCACAGTGATGAAATATTCAGACGAACTAGTAGAAACAGAGGGCCAAAATTGA	3350
Qy	3361	ATGCTATGCTTAAGTTAAGGGGTTTTCACAACCTAGAGCTATATAACAAAGCTCTCCGTGAA	3420
Db	3361	ATGCTATGCTTAAGTTAAGGGGTTTTCACAACCTAGAGCTATATAACAAAGCTCTCCGTGAA	3420
Qy	3421	GTAATTGTAAAGTCTCTGAATATAAAAAGCAAGAAATATAGAAAGTAGTTAGACTGTTA	3480
Db	3421	GTAATTGTAAAGTCTCTGAATATAAAAAGCAAGAAATATAGAAAGTAGTTAGACTGTTA	3480
Qy	3481	ATACAGTTTCTCTCCATATCTATTTTCAGATTAAGTACAGGCTATGGAGTACTC	3540
Db	3481	ATACAGTTTCTCTCCATATCTATTTTCAGATTAAGTACAGGCTATGGAGTACTC	3540
Qy	3541	ATGCATCTCAGGTTTGTTGAGACACCTGATGAGCTGTATGATATGCTGTAATAAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTTGAGACACCTGATGAGCTGTATGATATGCTGTAATAAAGG	3600
Qy	3601	AAGATACTAGTTTGTGTAATATGACATTAAAGAAAGTTCTGCTGTTTAAAGCAAAAGCG	3660
Db	3601	AAGATACTAGTTTGTGTAATATGACATTAAAGAAAGTTCTGCTGTTTAAAGCAAAAGCG	3660
Qy	3661	TCCAGAAAGAGAGCTTAGAGAGAGTCTAAGCCCTTACACCATACATTTGGCTCAGG	3720
Db	3661	TCCAGAGAGAGAGCTTAGAGAGAGTCTAAGCCCTTACACCATACATTTGGCTCAGG	3720
Qy	3721	GTTACGAGAGGGGGCCAAATTTAGAGTCCGCAAGAGAACTTATCTAGTGGAGATG	3780
Db	3721	GTTACCGAGAGGGGGCCAAATTTAGAGTCCGCAAGAGAACTTATCTAGTGGAGATG	3780
Qy	3781	AAGAGCTTCCCTGCTCCCAACACTGTTATTGTTAAAGTAACAATATACCTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTCCCAACACTGTTATTGTTAAAGTAACAATATACCTCTCAGT	3840
Qy	3841	CTACTAGGCATACACCGCTTGCTACCGAGTGTCTGTAAAGAACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCATACACCGCTTGCTACCGAGTGTCTGTAAAGAACACAGAGAGAAATTTAT	3900
Qy	3901	TATCATTTGAAGATAGCTTAAATAGTGTGAGTACACAGGTAATATGSCAAAGCATCTC	3960
Db	3901	TATCATTTGAAGATAGCTTAAATAGTGTGAGTACACAGGTAATATGSCAAAGCATCTC	3960
Qy	3961	AGGAACATCACCTTAGTAGAGAGAAACAAATGTCTGCTGTTTCTTCACAGTCA	4020
Db	3961	AGGAACATCACCTTAGTAGAGAGAAACAAATGTCTGCTGTTTCTTCACAGTCA	4020
Qy	4021	GTTGAATTGGAAGACTTGACTGCAATATACAACACCAGAGTCTTTCTTGATGGTTCTT	4080
Db	4021	GTTGAATTGGAAGACTTGACTGCAATATACAACACCAGAGTCTTTCTTGATGGTTCTT	4080
Qy	4081	CCAAACAAATAGAGGCATCACTGCTGAAGAGCCAGAGGATGTGTGAGTGACAAAGAAATGG	4140
Db	4081	CCAAACAAATAGAGGCATCACTGCTGAAGAGCCAGAGGATGTGTGAGTGACAAAGAAATGG	4140
Qy	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAGAAATATATACAAAGAGCAAAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAGAAATATATACAAAGAGCAAAAGCA	4200
Qy	4201	TGATTTCAAACCTTAGGTGAAGCAGCATCTGGGGTGAGAGTGAACAAGCGCTCTGTAAG	4260
Db	4201	TGATTTCAAACCTTAGGTGAAGCAGCATCTGGGGTGAGAGTGAACAAGCGCTCTGTAAG	4260
Qy	4261	ACTGCTACAGGGCTATCTCTCTCAGAGTACATTTTAACCACTACAGAGGGGATACATGCG	4320
Db	4261	ACTGCTACAGGGCTATCTCTCTCAGAGTACATTTTAACCACTACAGAGGGGATACATGCG	4320
Qy	4321	AACATTAAGCTGATTAAGAGCTCCACAGAGAAATGGGTAAGTGAAGCTGTATTAGAACGC	4380
Db	4321	AACATTAAGCTGATTAAGAGCTCCACAGAGAAATGGGTAAGTGAAGCTGTATTAGAACGC	4380
Qy	4381	ATGGAGCCACGCTTCTAACAGCTACCCCTTCATATAGTAGACTCTTCCCTTGAGG	4440

Db 4381 ATGGGACCAAGCCTTCTTAACAGCTACCTTCATCATATAGTACTCTTCTGCCCTTGAGG 4440  
Qy 4441 ACCTGCAAAATCCAGAACAAAGCACATCCGAAAAAGAGATTAATTAATTCACAGAAAAGTA 4500  
Db 4441 ACCTGCAAAATCCAGAACAAAGCACATCCGAAAAAGAGATTAATTAATTCACAGAAAAGTA 4500  
Qy 4501 GTGAATACCTTATTAAGCCAAATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAAGTGTGTG 4560  
Db 4501 GTGAATACCTTATTAAGCCAAATCCAGAAAGCCCTTCTGCTGACAAAGTTTGAAGTGTGTG 4560  
Qy 4561 CAGATAGTTTACCAAGTAAATAAAGAACAGAGAGTGGAAAGGTCATCCCTCTTAAT 4620  
Db 4561 CAGATAGTTTACCAAGTAAATAAAGAACAGAGAGTGGAAAGGTCATCCCTCTTAAT 4620  
Qy 4621 GCCCATCATTAAGATAGTGGTGTACATGCACAGTGTCTGGAGTCTTCCAGAAATAGAA 4680  
Db 4621 GCCCATCATTAAGATAGTGGTGTACATGCACAGTGTCTGGAGTCTTCCAGAAATAGAA 4680  
Qy 4681 ACTACCATCTCAAGAGAGACTCATTAAGTGTGTGATGTGGAGAGCAACAGCTGGAG 4740  
Db 4681 ACTACCATCTCAAGAGAGACTCATTAAGTGTGTGATGTGGAGAGCAACAGCTGGAG 4740  
Qy 4741 AGTGTGGGCCACAGATTTGACGGAAACATCTTACTGCGCAAGCAGATCTAGAGGAA 4800  
Db 4741 AGTGTGGGCCACAGATTTGACGGAAACATCTTACTGCGCAAGCAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACTGGAATCTGGAATCAGCCTCTTCTGTATGACCTGAACTGTGATCCTTCTG 4860  
Db 4801 CCCCTTACTGGAATCTGGAATCAGCCTCTTCTGTATGACCTGAACTGTGATCCTTCTG 4860  
Qy 4861 AAGACAGAGCCCAAGATCAGCTGCTGTGGCAACATACATCTTCAACCTCTGATTTGA 4920  
Db 4861 AAGACAGAGCCCAAGATCAGCTGCTGTGGCAACATACATCTTCAACCTCTGATTTGA 4920  
Qy 4921 AAGTCCCAATTTGAAGTTGACAGAAATCTGCCAGAGTCCAGCTGCTGCTACTACTG 4980  
Db 4921 AAGTCCCAATTTGAAGTTGACAGAAATCTGCCAGAGTCCAGCTGCTGCTACTACTG 4980  
Qy 4981 ATACTGCTGGGTATATGCAATGGAGAAAGTGTGACAGAGGAGAGAGCCAGATTTGACAG 5040  
Db 4981 ATACTGCTGGGTATATGCAATGGAGAAAGTGTGACAGAGGAGAGAGCCAGATTTGACAG 5040  
Qy 5041 CTTCAACAGAAAGGGTGAACAAAAGAAATGTCATGTGTGTGCTGCTGAGCCCAAGAG 5100  
Db 5041 CTTCAACAGAAAGGGTGAACAAAAGAAATGTCATGTGTGTGCTGCTGAGCCCAAGAG 5100  
Qy 5101 AATTTATGCTGCTGACAGTTTGCAGAAAACACACATCACTTAACTAATTA 5160  
Db 5101 AATTTATGCTGCTGACAGTTTGCAGAAAACACACATCACTTAACTAATTA 5160  
Qy 5161 CTGAAGAGACTCATGTGTGTATGAAAACAGATGCTGATGTTGTGTGTAACGGGACAC 5220  
Db 5161 CTGAAGAGACTCATGTGTGTATGAAAACAGATGCTGATGTTGTGTGTAACGGGACAC 5220  
Qy 5221 TGAATATTTTCTAGGAATTCGGGAGAGAAATGGTATGATTAATTTCCGGGTGACC 5280  
Db 5221 TGAATATTTTCTAGGAATTCGGGAGAGAAATGGTATGATTAATTTCCGGGTGACC 5280  
Qy 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTCAGAGGAAATGTGG 5340  
Db 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTCAGAGGAAATGTGG 5340  
Qy 5341 TCATATGGAAGAAACCAACCAAGGTCCTCAAGGAGAGATCCAGAGACGAAGATCT 5400  
Db 5341 TCATATGGAAGAAACCAACCAAGGTCCTCAAGGAGAGATCCAGAGACGAAGATCT 5400  
Qy 5401 TCGGGGGGTAGAAATGCTGTGATGGGCCCTTCAACAACATCCCAAGATCAATG 5460  
Db 5401 TCGGGGGGTAGAAATGCTGTGATGGGCCCTTCAACAACATCCCAAGATCAATG 5460  
Qy 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
Db 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520

Qy 5521 GCACAGGTGTCACCAATTTGTGTGTGTGACAGCCAGATGCTGGAGACAGACATGGCT 5580  
Db 5521 GCACAGGTGTCACCAATTTGTGTGTGTGACAGCCAGATGCTGGAGACAGACATGGCT 5580  
Qy 5581 TCCATGCAATTTGGGACATATGTGTGAGGCACACTGTGTGTGTGTGTGTGTGTGTGTGT 5640  
Db 5581 TCCATGCAATTTGGGACATATGTGTGAGGCACACTGTGTGTGTGTGTGTGTGTGTGTGT 5640  
Qy 5641 GTGTGACACTCTACAGATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700  
Db 5641 GTGTGACACTCTACAGATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 12  
AR007333 AR007333 5711 bp DNA PAT 04-DEC-1998  
LOCUS AR007333  
DEFINITION Sequence 1 from patent US 5750400.  
ACCESSION AR007333  
NID 93966817  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,  
Schelter, D.B. and Zeng, B.  
Coding sequences of the human BRCA1 gene  
JOURNAL Patent: US 5750400-A 1 12-MAY-1998;  
FEATURES  
location/Qualifiers  
source 1..5711  
BASE COUNT 1953 a 1099 c 1277 g 1382 t  
ORIGIN

Query Match 99.8%; Score 5701.4; DB 6; Length 5711;  
Best Local Similarity 99.98%; Pred. No. 0;  
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AGCTCGTGAAGTCTCTGAGACCCGACACAGAGCTGTGGGTTCTCAGATTAAGTGGCC 60  
Db 1 AGCTCGTGAAGTCTCTGAGACCCGACACAGAGCTGTGGGTTCTCAGATTAAGTGGCC 60  
Qy 61 CTTGCGGTGAGAGGCTTACCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120  
Db 61 CTTGCGGTGAGAGGCTTACCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120  
Qy 121 TGAATTTATGCTCTTCCGCTTGAAGAAGTACAAATGCTAATGCTATGCAAGAAA 180  
Db 121 TGAATTTATGCTCTTCCGCTTGAAGAAGTACAAATGCTAATGCTATGCAAGAAA 180  
Qy 121 TGAATTTATGCTCTTCCGCTTGAAGAAGTACAAATGCTAATGCTATGCAAGAAA 180  
Db 121 TGAATTTATGCTCTTCCGCTTGAAGAAGTACAAATGCTAATGCTATGCAAGAAA 180  
Qy 181 TCTTAGAGTGTCCATCTGTGTGAGTTGATCAAGAACTCTTCCAAAGTGTGACC 240  
Db 181 TCTTAGAGTGTCCATCTGTGTGAGTTGATCAAGAACTCTTCCAAAGTGTGACC 240  
Qy 241 ACATATTTTGAAGAAATTTGATGCTGAACTTCTCAACCAAGAAAGGAGGCTTACAGT 300  
Db 241 ACATATTTTGAAGAAATTTGATGCTGAACTTCTCAACCAAGAAAGGAGGCTTACAGT 300  
Qy 301 GTCTTTATGTAAGATGATTAATTAACCAAGAGGCTTACCAAGAAAGTACAGATTTAGTC 360  
Db 301 GTCTTTATGTAAGATGATTAATTAACCAAGAGGCTTACCAAGAAAGTACAGATTTAGTC 360  
Qy 361 AACTGTGTAAGAGATTAATTAATTTGCTTTTCAAGCTTCAACAGAGTTGGAGT 420  
Db 361 AACTGTGTAAGAGATTAATTAATTTGCTTTTCAAGCTTCAACAGAGTTGGAGT 420  
Qy 421 ATGCAAAACAGCTTAATTTTGGCAAAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480



Db 421 ATGCAAAAGCTATATTTTGGAAAAAGAAAAATACCTCTCTTAACATCTTAAGATG 480  
 Oy 481 AAGTTTCATCATCCAAAGATATGGGCTACAGAAACCGTCCAAAAAGCTTCTACAGAGTG 540  
 Db 481 AAGTTTCATCATCCAAAGATATGGGCTACAGAAACCGTCCAAAAAGCTTCTACAGAGTG 540  
 Oy 541 AACCCGAAAAATCCTTCTCTGCGAGAAACCATCTCAAGTCTCAACTCTCTAACTTTGAA 600  
 Db 541 AACCCGAAAAATCCTTCTCTGCGAGAAACCATCTCAAGTCTCAACTCTCTAACTTTGAA 600  
 Oy 601 CGTGTGAACCTGTGAGCAAGCAAGCGGATCAACCTCAAAAGAGCTCTGCTCAATTG 660  
 Db 601 CGTGTGAACCTGTGAGCAAGCAAGCGGATCAACCTCAAAAGAGCTCTGCTCAATTG 660  
 Oy 661 AATTGGAGTCGATCTCTCTGAGATACCGTTAATAGGCAACTATTGCAAGTGGAG 720  
 Db 661 AATTGGAGTCGATCTCTCTGAGATACCGTTAATAGGCAACTATTGCAAGTGGAG 720  
 Oy 721 ATCAGAATTTGTACAAATCACCCCTCAAGAACAGGAGTAAATCAGTTGATTCG 780  
 Db 721 ATCAGAATTTGTACAAATCACCCCTCAAGAACAGGAGTAAATCAGTTGATTCG 780  
 Oy 781 CAAAAAGGCTGCTGTGATTTTCTGAGACGGATTAACCAATCTGAACTCATCAAC 840  
 Db 781 CAAAAAGGCTGCTGTGATTTTCTGAGACGGATTAACCAATCTGAACTCATCAAC 840  
 Oy 841 CCAGTAATATATGATTGGAACACCACTGAGAAACGCTGAGCTGAGAGCATCCAGAAAGT 900  
 Db 841 CCAGTAATATATGATTGGAACACCACTGAGAAACGCTGAGAGCATCCAGAAAGT 900  
 Oy 901 ATCAGGATGTTCTGTTCAAACTTGACATGTGAGCCATGTGGCAACAAATCTCATGCCA 960  
 Db 901 ATCAGGATGTTCTGTTCAAACTTGACATGTGAGCCATGTGGCAACAAATCTCATGCCA 960  
 Oy 961 GCTCATTTACAGATGAGAAACGACATTTATCTACATAAAGCAAGATGTGAGAA 1020  
 Db 961 GCTCATTTACAGATGAGAAACGACATTTATCTACATAAAGCAAGATGTGAGAA 1020  
 Oy 1021 AAGCTGAATTTCTGTAATAAAGCAAAACGCTGCTTAGCAAGAGCAACATAACAGAT 1080  
 Db 1021 AAGCTGAATTTCTGTAATAAAGCAAAACGCTGCTTAGCAAGAGCAACATAACAGAT 1080  
 Oy 1081 GGGCTGGAAGTAGGAAACATGTATGATAGGCGGACTCCAGCACAGAAAAAAGTAG 1140  
 Db 1081 GGGCTGGAAGTAGGAAACATGTATGATAGGCGGACTCCAGCACAGAAAAAAGTAG 1140  
 Oy 1141 ATCTGAATGCTGATCCCTGCTGTGAGAAAAAAGATGGAATAGAGAAACGCGCATCT 1200  
 Db 1141 ATCTGAATGCTGATCCCTGCTGTGAGAAAAAAGATGGAATAGAGAAACGCGCATCT 1200  
 Oy 1201 CAGAGAACTCTGAGATCTAGATGTTCTTGTGATTAACATAATAGCAGATTCAGA 1260  
 Db 1201 CAGAGAACTCTGAGATCTAGATGTTCTTGTGATTAACATAATAGCAGATTCAGA 1260  
 Oy 1261 AAGTTAATGAGTGGTTTCCAGAGATGATGAACTGTAGGTTCTGATGACTCATGATG 1320  
 Db 1261 AAGTTAATGAGTGGTTTCCAGAGATGATGAACTGTAGGTTCTGATGACTCATGATG 1320  
 Oy 1321 GGGATCTGAANTCAAAATGCCAAAGTAGCTGATGTTGAGACCTTAAATGAGTAGT 1380  
 Db 1321 GGGATCTGAANTCAAAATGCCAAAGTAGCTGATGTTGAGACCTTAAATGAGTAGT 1380  
 Oy 1381 AATATTCGTCTCTCAGAGAAATAGACTTACTGCGCAGTATCTCATGAGGCTTTAA 1440  
 Db 1381 AATATTCGTCTCTCAGAGAAATAGACTTACTGCGCAGTATCTCATGAGGCTTTAA 1440  
 Oy 1441 TATGTAAAGTGAAGAGTTCACCTCAAAATCAGTAGAGAGTAAATTTGAAGCAAAATAT 1500  
 Db 1441 TATGTAAAGTGAAGAGTTCACCTCAAAATCAGTAGAGAGTAAATTTGAAGCAAAATAT 1500  
 Oy 1501 TTGGAAAAACCTATCGGAGAGAGAGGACCTCCCAACTTAAGCATGTACGAAATC 1560  
 Db 1501 TTGGAAAAACCTATCGGAGAGAGAGGACCTCCCAACTTAAGCATGTACGAAATC 1560

Db 1501 TTGGAAAAACCTATCGGAGAGAGAGGACCTCCCAACTTAAGCATGTACGAAATC 1560  
 Oy 1561 TAAATATAGAGACTTTTGTACTGAGCCACAGATTAATCAAGAGCTGCCCTACAATA 1620  
 Db 1561 TAAATATAGAGACTTTTGTACTGAGCCACAGATTAATCAAGAGCTGCCCTACAATA 1620  
 Oy 1621 AATTAAACCTTAAAGAGACTACATCAGGCCCTTCAACCTCGAGATTTTCAAGAAAG 1680  
 Db 1621 AATTAAACCTTAAAGAGACTACATCAGGCCCTTCAACCTCGAGATTTTCAAGAAAG 1680  
 Oy 1681 CAGATTTGGAGTTCAAAAGACTCCTGAAATGATTAATCAGGAACTTAACCAAGAGC 1740  
 Db 1681 CAGATTTGGAGTTCAAAAGACTCCTGAAATGATTAATCAGGAACTTAACCAAGAGC 1740  
 Oy 1741 AGAATGTCAGTGAATATATCTAATAATAGTGTGATGAGATTAACCAAAAGGTGAT 1800  
 Db 1741 AGAATGTCAGTGAATATATCTAATAATAGTGTGATGAGATTAACCAAAAGGTGAT 1800  
 Oy 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCCTGCAAGAAAAAGATCTGTTCA 1860  
 Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCCTGCAAGAAAAAGATCTGTTCA 1860  
 Oy 1861 AAAGGAAAGCTGAACCTTAAGCAGAGTATAGCAATATGGAATGGAATTAATATCC 1920  
 Db 1861 AAAGGAAAGCTGAACCTTAAGCAGAGTATAGCAATATGGAATGGAATTAATATCC 1920  
 Oy 1921 ACAATTTCAAAAGCACTTAAAAAGATAGGCTGAGAGAGAGTCTTCTACAGCATATTC 1980  
 Db 1921 ACAATTTCAAAAGCACTTAAAAAGATAGGCTGAGAGAGAGTCTTCTACAGCATATTC 1980  
 Oy 1981 ATGGCTTGAACCTGATGATCTGATGAAATCTAAGCCCACTTAATTTGTAATTTGCAA 2040  
 Db 1981 ATGGCTTGAACCTGATGATCTGATGAAATCTAAGCCCACTTAATTTGTAATTTGCAA 2040  
 Oy 2041 TTGATAGTGTTCAGAGGTAGAGATTAAGAAAAAAGTAAACCAATAGGCACTCA 2100  
 Db 2041 TTGATAGTGTTCAGAGGTAGAGATTAAGAAAAAAGTAAACCAATAGGCACTCA 2100  
 Oy 2101 GGCACAGCAGAAACCTTACACTCATGGAAGTAAAGAACTGCAACTGAGCCAAAGAA 2160  
 Db 2101 GGCACAGCAGAAACCTTACACTCATGGAAGTAAAGAACTGCAACTGAGCCAAAGAA 2160  
 Oy 2161 GTAACAGCCAAATGAAAGACGAAATGAAAGACATGAGATGATCTTCCAGAGCTGA 2220  
 Db 2161 GTAACAGCCAAATGAAAGACGAAATGAAAGACATGAGATGATCTTCCAGAGCTGA 2220  
 Oy 2221 AGTTAACAATGACACCTGCTTCTTACTAGTGTTCAAATACCAAGTAAAGAT 2280  
 Db 2221 AGTTAACAATGACACCTGCTTCTTACTAGTGTTCAAATACCAAGTAAAGAT 2280  
 Oy 2281 TTGTCATCTCTAGCCTTCCAGAGAGAAAAAGAAAGTAAAGTAAAGT 2340  
 Db 2281 TTGTCATCTCTAGCCTTCCAGAGAGAAAAAGAAAGTAAAGTAAAGT 2340  
 Oy 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAAGAGGTTTGCAACTG 2400  
 Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAAGAGGTTTGCAACTG 2400  
 Oy 2401 AAAGATGCTGAGAGTGAAGTATTTTCAATGATGATGATGATGATGATGATGATG 2460  
 Db 2401 AAAGATGCTGAGAGTGAAGTATTTTCAATGATGATGATGATGATGATGATGATG 2460  
 Oy 2461 AAAGATCTCTCTACTGGAAGTATGACACTGAGGAAAGGCAAAAAAGCAAAATAT 2520  
 Db 2461 AAAGATCTCTCTACTGGAAGTATGACACTGAGGAAAGGCAAAAAAGCAAAATAT 2520  
 Oy 2521 GTGTGAGTCACTGTGACGACATTTGAAAAACCAAGGCACTAATCATGTTGTCCAAAG 2580  
 Db 2521 GTGTGAGTCACTGTGACGACATTTGAAAAACCAAGGCACTAATCATGTTGTCCAAAG 2580  
 Oy 2581 ATATATAGAAATGACACGAAGGCTTAAAGTATCATGTTGGGACATGAAGTTAACACAGTC 2640  
 Db 2581 ATATATAGAAATGACACGAAGGCTTAAAGTATCATGTTGGGACATGAAGTTAACACAGTC 2640

OY	2641	GGAAAAACAGCATAGAAATGGAAGAAAGTGACATTGAGCTCAGTATTTTGGCAATACAT	2700
Db	2641	GGAAAAACAGCATAGAAATGGAAGAAAGTGAACTGATGCTCAGTATTTTGGCAATACAT	2700
OY	2701	TCAGAGTTTCAAAAGCGGCAGCTCATTTTGTCTGTGTTTCAAAATCCAGAAATCCAGAGAG	2760
Db	2701	TCAGAGTTTCAAAAGCGGCAGCTCATTTTGTCTGTGTTTCAAAATCCAGAAATCCAGAGAG	2760
OY	2761	AATGTGCACATTCTCTGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Db	2761	AATGTGCACATTCTCTGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
OY	2821	TTGAATGTGAACAAAGGAAGAAATATAGGAAGAAATGACTTCATATCAAGCTGAC	2880
Db	2821	TTGAATGTGAACAAAGGAAGAAATATAGGAAGAAATGACTTCATATCAAGCTGAC	2880
OY	2881	AGACAGTTAATATCACTGACAGGCTTCTGTGTGGTCAAGAAAGATAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGACAGGCTTCTGTGTGGTCAAGAAAGATAGCCAGTTGATA	2940
OY	2941	ATGCCAAATCTACTATCAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCCAAATCTACTATCAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGGCA	3000
OY	3001	ACGAAACTGGACTCATTACTCCCAATTAACATGGACTTTTACAAGAACCATATGATATAC	3060
Db	3001	ACGAAACTGGACTCATTACTCCCAATTAACATGGACTTTTACAAGAACCATATGATATAC	3060
OY	3061	CACCACTTTTCCCATCAAGTCACTTTGTCTTAAACTTAAATGTAGAAAAATCTGCTAGAG	3120
Db	3061	CACCACTTTTCCCATCAAGTCACTTTGTCTTAAACTTAAATGTAGAAAAATCTGCTAGAG	3120
OY	3121	AAAACCTTGGAGAACATTCATATGCACCTGAGAGAGAAATGGGAAATGAGAACCTTGCAA	3180
Db	3121	AAAACCTTGGAGAACATTCATATGCACCTGAGAGAGAAATGGGAAATGAGAACCTTGCAA	3180
OY	3181	GTAACAGTGAACACATTTAGCCGTAAATACATTTAGAAAAATGTTTTTAAAGAACCAAGCT	3240
Db	3181	GTAACAGTGAACACATTTAGCCGTAAATACATTTAGAAAAATGTTTTTAAAGAACCAAGCT	3240
OY	3241	CAAGCAATTTTATGAAAGTGGTCCAGTACTAATGAAGAGGGGCTCCAGATTTAATGAAA	3300
Db	3241	CAAGCAATTTTATGAAAGTGGTCCAGTACTAATGAAGAGGGGCTCCAGATTTAATGAAA	3300
OY	3301	TAGGTTCCAGTGTGAAAAACATTTCAAGCAGAACATAGGTACAAAACAGAGGCCAAATTTGA	3360
Db	3301	TAGGTTCCAGTGTGAAAAACATTTCAAGCAGAACATAGGTACAAAACAGAGGCCAAATTTGA	3360
OY	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCCTTAAACAAAGTCTTCTGGA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCCTTAAACAAAGTCTTCTGGA	3420
OY	3421	GTAATGTAGCACTCTGAAAAATAAAAAAGCAAGATTTGAAGAGTAGTTCAGACTGTTA	3480
Db	3421	GTAATGTAGCACTCTGAAAAATAAAAAAGCAAGATTTGAAGAGTAGTTCAGACTGTTA	3480
OY	3481	ATACAGATTTCCTCCATATCTGATTTCAATTAACATTAAGCAACAGCCATATGGAAAGTAGTC	3540
Db	3481	ATACAGATTTCCTCCATATCTGATTTCAATTAACATTAAGCAACAGCCATATGGAAAGTAGTC	3540
OY	3541	ATGCATCTCAGGTTTCTTGAAACACCTGATATCACTGTTAGATGAGTGGTGAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTTCTTGAAACACCTGATATCACTGTTAGATGAGTGGTGAATTAAGG	3600
OY	3601	AAGATACAGTTTGGTGAAGAAATGAATTAAGGAAGATTCGTGTTTTTATAGCAAAAGCG	3660
Db	3601	AAGATACAGTTTGGTGAAGAAATGAATTAAGGAAGATTCGTGTTTTTATAGCAAAAGCG	3660
OY	3661	TCCAGAGAGAGAGCTTAGCAGAGAGTCTTAGCCCTTACCCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAGAGAGAGCTTAGCAGAGAGTCTTAGCCCTTACCCATACACATTTGGCTCAGG	3720

QY	3721	GTACCGAAGAGGGGCCAAGAATTAGAGTCTCAGAAAGAACTTATCTAGTAGATG	3780
Db	3721	GTATACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAAGAACTTATCTAGTAGATG	3780
QY	3781	AGAGCTTCCCTGCTCCCAACACTGTGTAATTTGTAAGTAACAAATTAACCTTCAGT	3840
Db	3781	AGAGCTTCCCTGCTCCCAACACTGTGTAATTTGTAAGTAACAAATTAACCTTCAGT	3840
QY	3841	CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTAAAGACAGAGGAAATTTAT	3900
Db	3841	CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTAAAGACAGAGGAAATTTAT	3900
QY	3901	TATCATTTAABAATAGCTTAAATGACTGCAGTACCAGGTAATATTGGCAAGGATCTC	3960
Db	3901	TATCATTTAABAATAGCTTAAATGACTGCAGTACCAGGTAATATTGGCAAGGATCTC	3960
QY	3961	AGGAACATCACCTTAGAGAGAAACAAATGTTGCTAGCTGTGTTTCTTCACAGTGCA	4020
Db	3961	AGGAACATCACCTTAGAGAGAAACAAATGTTGCTAGCTGTGTTTCTTCACAGTGCA	4020
QY	4021	GTGATTTGGAAGACTTACGTACGCAAAATACAAACACCAGATCCCTTCTGATTGGTCTT	4080
Db	4021	GTGATTTGGAAGACTTACGTACGCAAAATACAAACACCAGATCCCTTCTGATTGGTCTT	4080
QY	4081	CCAAACAATATGAGGCATCACTCTGAAACCCAGGAGTGTGCTGAGTACAGCAATTTGG	4140
Db	4081	CCAAACAATATGAGGCATCACTCTGAAACCCAGGAGTGTGCTGAGTACAGCAATTTGG	4140
QY	4141	TTTCAGATGATGAAGAAAGAGGAACGGGCTTGGAAGAAATTAATCAAGAACGAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGGAACGGGCTTGGAAGAAATTAATCAAGAACGAAGCA	4200
QY	4201	TGATTTCAAATCTTAGTGAAGAGCAGCATCTGGGTGTGAGAGTGAACCAAGCCTCTAG	4260
Db	4201	TGATTTCAAATCTTAGTGAAGAGCAGCATCTGGGTGTGAGAGTGAACCAAGCCTCTAG	4260
QY	4261	ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAACCACTCAGCAGAGGATACCATGC	4320
Db	4261	ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAACCACTCAGCAGAGGATACCATGC	4320
QY	4321	AACATTAACCTGATTAACCTCCAGCAGAAATGGCTGAACATAAAGCTGTGTAACAGC	4380
Db	4321	AACATTAACCTGATTAACCTCCAGCAGAAATGGCTGAACATAAAGCTGTGTAACAGC	4380
QY	4381	ATGGAGAGCAGCCTTCTTAACAGCTTCCATATAAAGTACCTCTCCCTTAGG	4440
Db	4381	ATGGAGAGCAGCCTTCTTAACAGCTTCCATATAAAGTACCTCTCCCTTAGG	4440
QY	4441	ACCTGCGAAATCCAGAAACAAAGCAGCATCGAAAAAGACAGTATTAACTTCACAGAAAGTA	4500
Db	4441	ACCTGCGAAATCCAGAAACAAAGCAGCATCGAAAAAGACAGTATTAACTTCACAGAAAGTA	4500
QY	4501	GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCTTCTGCTGACAAAGTTGAGGTCTG	4560
Db	4501	GTGAATACCTTATTAAGCCAGAAATCCAGAAAGCCTTCTGCTGACAAAGTTGAGGTCTG	4560
QY	4561	CAGATTACTTACACAGTAAAAAATAAAGAACAGAGGTGGAAGGTCATCCCTCTTAAT	4620
Db	4561	CAGATTACTTACACAGTAAAAAATAAAGAACAGAGGTGGAAGGTCATCCCTCTTAAT	4620
QY	4621	GCCCATCATTAGATAGTAGGTGGTATACATCACAGTGTGCTGGAGTCTTCAGAAATGA	4680
Db	4621	GCCCATCATTAGATAGTAGGTGGTATACATCACAGTGTGCTGGAGTCTTCAGAAATGA	4680
QY	4681	ACTATCCATCTCAAGAGAGGACTCATTAAGGTGTGATGTGAGAGAGCAACAGCTGGAAG	4740
Db	4681	ACTATCCATCTCAAGAGAGGACTCATTAAGGTGTGATGTGAGAGAGCAACAGCTGGAAG	4740
QY	4741	AGTGTGGGACACAGATTTGAGAGAAACATCTTACTTGCAGAGCAGAGTCTAGAGGAA	4800
Db	4741	AGTGTGGGACACAGATTTGAGAGAAACATCTTACTTGCAGAGCAGAGTCTAGAGGAA	4800
QY	4801	CCCCCTTACCTGGAATGTGGAATAGCCCTTCTTCGATGAGACCTCGAATCTGATCTTCTG	4860

```

Db 4801 CCCCTACTGGAATTCGAATTCACCTCTTCTCTGATGACCTCGAATCTGATCTTCTG 4860
Qy 4861 AAGACAGAGCCCGAGAGTACAGCTGCTGTTGGCAACATACATCTTCAACCTCTGCATGA 4920
Db 4861 AAGACAGAGCCCGAGAGTACAGCTGCTGTTGGCAACATACATCTTCAACCTCTGCATGA 4920
Qy 4921 AAGTCCCCCAATTGAAGTTCAGATCTGCCAGAGTCCAGTCTGCTCATACTACTG 4980
Db 4921 AAGTCCCCCAATTGAAGTTCAGATCTGCCAGAGTCCAGTCTGCTCATACTACTG 4980
Qy 4981 ATACTGCTGGGTATTAATTCATGAGAAAGTGTGAGAGGAGAGAGCAATTTGAGAG 5040
Db 4981 ATACTGCTGGGTATTAATTCATGAGAAAGTGTGAGAGGAGAGAGCAATTTGAGAG 5040
Qy 5041 CTTCACAGAAAGGGTCAACAAAGAAATGTCATGCTGCTGCTGCTGAGCCAGAG 5100
Db 5041 CTTCACAGAAAGGGTCAACAAAGAAATGTCATGCTGCTGCTGAGCCAGAGAG 5100
Qy 5101 AATTATGCTGCTGACAGATTTGCCAGAAACACCATCATCTTAACTAATCTAATTA 5160
Db 5101 AATTATGCTGCTGACAGATTTGCCAGAAACACCATCATCTTAACTAATCTAATTA 5160
Qy 5161 CTGAGAGACTACTGATGTTGTTATGAAACAGATGCTGATTTGTTGTAAGGAGAC 5220
Db 5161 CTGAGAGACTACTGATGTTGTTATGAAACAGATGCTGATTTGTTGTAAGGAGAC 5220
Qy 5221 TGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGTATTTCTGCTGAGACC 5280
Db 5221 TGAATATTTTCTAGAAATTCGGAGAGAAATGGGTAGTATTTCTGCTGAGACC 5280
Qy 5281 AGCTATTTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGG 5340
Db 5281 AGCTATTTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGG 5340
Qy 5341 TCATGAGAGAAACACCAAGGTCGAAAGAGAGAGAGATCCAGAGAGAGAAAGATCT 5400
Db 5341 TCATGAGAGAAACACCAAGGTCGAAAGAGAGAGAGATCCAGAGAGAGAAAGATCT 5400
Qy 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGCCCTTACCAGATGCCAGATCAACTGG 5460
Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGCCCTTACCAGATGCCAGATCAACTGG 5460
Qy 5461 AATGATGCTACAGCTGTGCTGCTTCTGTGTGAGAGAGCTTTCATCAACCTTG 5520
Db 5461 AATGATGCTACAGCTGTGCTGCTTCTGTGTGAGAGAGCTTTCATCAACCTTG 5520
Qy 5521 GCACAGGTGTCACCAATTTGTTGTTGTCAGCAGATGCTGAGAGAGAGACATGGCT 5580
Db 5521 GCACAGGTGTCACCAATTTGTTGTTGTCAGCAGATGCTGAGAGAGAGACATGGCT 5580
Qy 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGAGTGGTGTGACA 5640
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGAGTGGTGTGACA 5640
Qy 5641 GTGTAGCACTTACCAAGTCCAGAGAGTGAACACTTACCTATACCCAGATCCCCACA 5700
Db 5641 GTGTAGCACTTACCAAGTCCAGAGAGTGAACACTTACCTATACCCAGATCCCCACA 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

```

## RESULT 13

```

LOCUS 159546 5711 bp DNA PAT 15-AUG-1997
DEFINITION Sequence 1 from patent US 5654155.
ACCESSION 159546
NID 92478178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

```

```

REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J.,
Schelter,D.B., and Zeng,B.
TITLE Consensus sequence of the human BRCA1 gene
JOURNAL Patent: US 5654155-A, 1 05-AUG-1997;
FEATURES
    source
        1. 5711
            /organism="unknown"
BASE COUNT 1953 a 1099 c 1277 g 1382 t
ORIGIN
Query Match 99.8%; Score 5701.4; DB 6; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 AGTCGCTGAGACTTCTGAGACCCCGACACGCTGTGGGTTCTCAGATTAAGTGGCC 60
Db 1 AGTCGCTGAGACTTCTGAGACCCCGACACGCTGTGGGTTCTCAGATTAAGTGGCC 60
Qy 61 CCTCGCTCAGAGAGGCTTCAACCTCTGCTGTGGTAAAGTTCATGGAACAGAAAGAA 120
Db 61 CCTCGCTCAGAGAGGCTTCAACCTCTGCTGTGGTAAAGTTCATGGAACAGAAAGAA 120
Qy 121 TGAATTAATCTGCTTCTGCGCTTGAGAGATGACAAATGTCATTAAATGCTATGAGAAAA 180
Db 121 TGAATTAATCTGCTTCTGCGCTTGAGAGATGACAAATGTCATTAAATGCTATGAGAAAA 180
Qy 181 TCTTAGAGTGTCCCATCTGCTGTGAGATGATCAAGAAACCTGTCTCCAAAGTGTACC 240
Db 181 TCTTAGAGTGTCCCATCTGCTGTGAGATGATCAAGAAACCTGTCTCCAAAGTGTACC 240
Qy 241 ACATATTTTGAATTTTGCATGCTGAACCTTCAACACAGAAAGAGGCTTCAAGT 300
Db 241 ACATATTTTGAATTTTGCATGCTGAACCTTCAACACAGAAAGAGGCTTCAAGT 300
Qy 301 GTCTTTATGTAAGATGATTAACAAAGAGAGAGAGAGAGAGAGAGAGATTAAGTGC 360
Db 301 GTCTTTATGTAAGATGATTAACAAAGAGAGAGAGAGAGAGAGAGAGATTAAGTGC 360
Qy 361 AACTTGTGAAGAGCTATGAAATCATTTTGTCTTTCAGCTTGAACAGAGTTGGAGT 420
Db 361 AACTTGTGAAGAGCTATGAAATCATTTTGTCTTTCAGCTTGAACAGAGTTGGAGT 420
Qy 421 ATGCAACAGCTAATTTTGCAGAAAGAGAAATTAACCTGCTGAACATTAAGAGT 480
Db 421 ATGCAACAGCTAATTTTGCAGAAAGAGAAATTAACCTGCTGAACATTAAGAGT 480
Qy 481 AAGTTTCTATCATCAAGATGATGGGTACAGAAACCGTCCAAAGAGCTTCTACAGAGTG 540
Db 481 AAGTTTCTATCATCAAGATGATGGGTACAGAAACCGTCCAAAGAGCTTCTACAGAGTG 540
Qy 541 AACCCGAAATCTCTCTTCTGAGAGAAACAGTCTCATGTGCAACTCTTAACCTTGGAA 600
Db 541 AACCCGAAATCTCTCTTCTGAGAGAAACAGTCTCATGTGCAACTCTTAACCTTGGAA 600
Qy 601 CTGTGAGAACTCTGAGAGCAAGAGCAGGATATCAACCTCAAAAGAGCTGTACATTTG 660
Db 601 CTGTGAGAACTCTGAGAGCAAGAGCAGGATATCAACCTCAAAAGAGCTGTACATTTG 660
Qy 661 AATTGGATCTGATTTCTTGAAGATACCGTTAATTAAGGCAACTTATGCAAGTGGAG 720
Db 661 AATTGGATCTGATTTCTTGAAGATACCGTTAATTAAGGCAACTTATGCAAGTGGAG 720
Qy 721 ATCAAGATGTTTCAATCAACCCCTCAAGAGACCAAGGATGAATCAAGTTGGATTCTG 780
Db 721 ATCAAGATGTTTCAATCAACCCCTCAAGAGACCAAGGATGAATCAAGTTGGATTCTG 780
Qy 781 CAAAAAAGGCTGTGTAATTTTCTGAGAGGATGTAACAAATACTGAACATCATCAAC 840
Db 781 CAAAAAAGGCTGTGTAATTTTCTGAGAGGATGTAACAAATACTGAACATCATCAAC 840

```

QY 841 CCAATTAATGATTTGACACCACTGGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGT 900  
 DB 841 CCAATTAATGATTTGACACCACTGGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGT 900  
 QY 901 ATGAGGCTAGTCTGTTTCAAACTTGCATGTGAGCCATGTGGCAAAATACTCATGCCA 960  
 DB 901 ATGAGGCTAGTCTGTTTCAAACTTGCATGTGAGCCATGTGGCAAAATACTCATGCCA 960  
 QY 961 GCTCATTACAGCATGAGAACAGCAGTTTATTACTCCTAAAGACAAATGAATGTAGAAA 1020  
 DB 961 GCTCATTACAGCATGAGAACAGCAGTTTATTACTCCTAAAGACAAATGAATGTAGAAA 1020  
 QY 1021 AGGCTGAATCTGTAAATAAAGCAAAAGCGTGGTGTGCAAGAGCCCAATATACAT 1080  
 DB 1021 AGGCTGAATCTGTAAATAAAGCAAAAGCGTGGTGTGCAAGAGCCCAATATACAT 1080  
 QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCAGCAAAAAAGTAG 1140  
 DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCAGCAAAAAAGTAG 1140  
 QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAATGAAGCAAACTGCCATGCT 1200  
 DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAATGAAGCAAACTGCCATGCT 1200  
 QY 1201 CAGAGAACTCTAGAGATGATGAAATGTTCTTGATTAACCTAAATAGCAGCATTCAGA 1260  
 DB 1201 CAGAGAACTCTAGAGATGATGAAATGTTCTTGATTAACCTAAATAGCAGCATTCAGA 1260  
 QY 1261 AAGTTAATGAGTGTGTTTCCAGAACTGATGAACTGTGATGATGATGATGATGATGATG 1320  
 DB 1261 AAGTTAATGAGTGTGTTTCCAGAACTGATGAACTGTGATGATGATGATGATGATGATG 1320  
 QY 1321 GGGAGTCTGATCAAAATGCCAAAGTACTGATGATGATGATGATGATGATGATGATG 1380  
 DB 1321 GGGAGTCTGATCAAAATGCCAAAGTACTGATGATGATGATGATGATGATGATGATG 1380  
 QY 1381 AATATTCTGTTCTTCCAGAAATAGACTGATGATGATGATGATGATGATGATGATGATG 1440  
 DB 1381 AATATTCTGTTCTTCCAGAAATAGACTGATGATGATGATGATGATGATGATGATGATG 1440  
 QY 1441 TATGTAAAGTGAAGAGTCTCACTCAAACTAGTAGAGAGTATATGTAAGAACAAATAT 1500  
 DB 1441 TATGTAAAGTGAAGAGTCTCACTCAAACTAGTAGAGAGTATATGTAAGAACAAATAT 1500  
 QY 1501 TTGGGAAAACCTATCGGAAAGGCAAGCCCTCCCACTTAAGCCATGTAAGTGAATATC 1560  
 DB 1501 TTGGGAAAACCTATCGGAAAGGCAAGCCCTCCCACTTAAGCCATGTAAGTGAATATC 1560  
 QY 1561 TAATTAATGAGAGATTTGTTACTAGGACAGATATATACAGAGAGTCCCTCCCAATA 1620  
 DB 1561 TAATTAATGAGAGATTTGTTACTAGGACAGATATATACAGAGAGTCCCTCCCAATA 1620  
 QY 1621 AATTTAAAGCGTAAAGAGAGACCTATACATCAGGCTTCACTCTGAGAGATTTTATCAAG 1680  
 DB 1621 AATTTAAAGCGTAAAGAGAGACCTATACATCAGGCTTCACTCTGAGAGATTTTATCAAG 1680  
 QY 1681 CAGATTGGGAGTTCAGAAAGACCTCTGAATGATTAATCAGGAACTTACCAAGCGAGC 1740  
 DB 1681 CAGATTGGGAGTTCAGAAAGACCTCTGAATGATTAATCAGGAACTTACCAAGCGAGC 1740  
 QY 1741 AGAATGCTCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATG 1800  
 DB 1741 AGAATGCTCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATG 1800  
 QY 1801 CTAATTCAGATGAGAAAAATCTTAACCAATAGAACTCTGAAAAAGAAATCTCTTCA 1860  
 DB 1801 CTAATTCAGATGAGAAAAATCTTAACCAATAGAACTCTGAAAAAGAAATCTCTTCA 1860  
 QY 1861 AAACGAAAGCTGAACCTATATAGCAGCAGTATAGCAATATGGAATTAATTAATATCC 1920  
 DB 1861 AAACGAAAGCTGAACCTATATAGCAGCAGTATAGCAATATGGAATTAATTAATATCC 1920  
 QY 1921 ACAATTCAAAAAGCACTTAAAAAGATAGGCTGAGGAGAGAGTCTTCAACAGCATATTC 1980

DB 1921 ACAATTCAAAAAGCACTTAAAAAGATAGGCTGAGGAGAGAGTCTTCAACAGCATATTC 1980  
 QY 1981 ATGCGCTTGAACCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
 DB 1981 ATGCGCTTGAACCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
 QY 2041 TTGATAGTGTCTTACAGAGTGAAGAGATTAAGAAAAAAAGTAAACCAACCAATGCCAGTCA 2100  
 DB 2041 TTGATAGTGTCTTACAGAGTGAAGAGATTAAGAAAAAAAGTAAACCAACCAATGCCAGTCA 2100  
 QY 2101 GGCACAGAGAAACCTCAACTCATGGAAGTAAAGAACTGGAAGTGAAGGAGGAGGAGGAGG 2160  
 DB 2101 GGCACAGAGAAACCTCAACTCATGGAAGTAAAGAACTGGAAGTGAAGGAGGAGGAGGAGG 2160  
 QY 2161 GTAAACAGCCAAATGAAAGAGAGCAAGTAAAGAGATGACAGGATGATGATGATGATGATG 2220  
 DB 2161 GTAAACAGCCAAATGAAAGAGAGCAAGTAAAGAGATGACAGGATGATGATGATGATGATG 2220  
 QY 2221 AGTTAACAAATGACCTGTGTTCTTTTACTAAGTGTCAATACCAATGATGATGATGATGATG 2280  
 DB 2221 AGTTAACAAATGACCTGTGTTCTTTTACTAAGTGTCAATACCAATGATGATGATGATGATG 2280  
 QY 2281 TTGTCATTCCTAGGCTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340  
 DB 2281 TTGTCATTCCTAGGCTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340  
 QY 2341 CTAATTAATGCTGAAG 2400  
 DB 2341 CTAATTAATGCTGAAG 2400  
 QY 2401 AAAGATCTGTAAGAGATGAGCAGTATTTTCAATGATGATGATGATGATGATGATGATGATG 2460  
 DB 2401 AAAGATCTGTAAGAGATGAGCAGTATTTTCAATGATGATGATGATGATGATGATGATGATG 2460  
 QY 2461 AAAGATCTGTAAGAGATGAGCAGTATTTTCAATGATGATGATGATGATGATGATGATGATG 2520  
 DB 2461 AAAGATCTGTAAGAGATGAGCAGTATTTTCAATGATGATGATGATGATGATGATGATGATG 2520  
 QY 2521 GTGTGAGTCAAGTGTGAGCAGTATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
 DB 2521 GTGTGAGTCAAGTGTGAGCAGTATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
 QY 2581 ATATTAATTAATGACAG 2640  
 DB 2581 ATATTAATTAATGACAG 2640  
 QY 2641 GGGAAACAGCAGTAAAGTGAAG 2700  
 DB 2641 GGGAAACAGCAGTAAAGTGAAG 2700  
 QY 2701 TCAAGGTTTCAAGGCGGAGCAGTATTTGCTCTGTTTCAATCCAGAGAAATGAGAGAGAG 2760  
 DB 2701 TCAAGGTTTCAAGGCGGAGCAGTATTTGCTCTGTTTCAATCCAGAGAAATGAGAGAGAG 2760  
 QY 2761 AATGTGCAACATTTCTGCCCAGTCTGAGGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2820  
 DB 2761 AATGTGCAACATTTCTGCCCAGTCTGAGGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2820  
 QY 2821 TTGATAGTGAAG 2880  
 DB 2821 TTGATAGTGAAG 2880  
 QY 2881 AGACAGTATTAATCACTGAGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940  
 DB 2881 AGACAGTATTAATCACTGAGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940  
 QY 2941 ATGCCAAATGATATCAAG 3000  
 DB 2941 ATGCCAAATGATATCAAG 3000  
 QY 3001 AGCAACTGAGACTTATCTCCAAATTAACATGAGACTTTTAAACCAACCAATCTATATC 3060

Db 3001 ACGAAATGAGCTATCTCCAAATTAACATGACTTTACAAAACCATATCTATAC 3060  
OY 3061 CACCACTTTTCCCATCAAGTCATTTGTAAAACTAAATGTAAGAAAATCTCTAGAG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCATTTGTAAAACTAAATGTAAGAAAATCTCTAGAG 3120  
OY 3121 AAAACTTGGAGAACATTCATATGTCACCTGTAAGAGAAATGGAAATGAGACATTC 3180  
Db 3121 AAAACTTGGAGAACATTCATATGTCACCTGTAAGAGAAATGGAAATGAGACATTC 3180  
OY 3181 GTACAGTGAACAAATAGCCGTAATACATGATGAGAAAATGTTTTAAAGAACAGCT 3240  
Db 3181 GTACAGTGAACAAATAGCCGTAATACATGATGAGAAAATGTTTTAAAGAACAGCT 3240  
OY 3241 CAAGCAATATTAATGAAGTGGTCCAGTACTAATGAGTGGGCTCCAGTATTAATGAA 3300  
Db 3241 CAAGCAATATTAATGAAGTGGTCCAGTACTAATGAGTGGGCTCCAGTATTAATGAA 3300  
OY 3301 TAGTTCAGATGATGAAGAACATTCAGAGACACTAGTAGAAAACAGAGGCCAAAATTGA 3360  
Db 3301 TAGTTCAGATGATGAAGAACATTCAGAGACACTAGTAGAAAACAGAGGCCAAAATTGA 3360  
OY 3361 ATGCTATGCTTAATAGGGGTTTGCAACCTGAGGCTATAACAAAGCTTCCGGA 3420  
Db 3361 ATGCTATGCTTAATAGGGGTTTGCAACCTGAGGCTATAACAAAGCTTCCGGA 3420  
OY 3421 GTAATTGTAAGATCCTGAAATAAAAAGCAAGATATGAGAAGTATGTCAGACTGTT 3480  
Db 3421 GTAATTGTAAGATCCTGAAATAAAAAGCAAGATATGAGAAGTATGTCAGACTGTT 3480  
OY 3481 ATACAGATTTCTCTCATATCTGATTTGAGATACCTTAGAACAGCCTATGGAGATGTC 3540  
Db 3481 ATACAGATTTCTCTCATATCTGATTTGAGATACCTTAGAACAGCCTATGGAGATGTC 3540  
OY 3541 ATACATCTCGGTTGTGTCGAGACACCTGATGACCTGTAGATGATGGGAATTAAG 3600  
Db 3541 ATACATCTCGGTTGTGTCGAGACACCTGATGACCTGTAGATGATGGGAATTAAG 3600  
OY 3601 AAGATACTAGTTCGTAAGAAATGACATTAAGGAAATTCGCTGTTTTAGCAAAAGCG 3660  
Db 3601 AAGATACTAGTTCGTAAGAAATGACATTAAGGAAATTCGCTGTTTTAGCAAAAGCG 3660  
OY 3661 TCCAGAAAGAGAGCTTAGCAGAGAGTCCTAGCCCTTACCCATACACATTTGGCTCAG 3720  
Db 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCCTAGCCCTTACCCATACACATTTGGCTCAG 3720  
OY 3721 GTTACGAGAGAGGGGCCAAGAAATAGAGCTCAGAGAGAACTATCTAGTGAAGATG 3780  
Db 3721 GTTACGAGAGAGGGGCCAAGAAATAGAGCTCAGAGAGAACTATCTAGTGAAGATG 3780  
OY 3781 AAGAGCTTCCTGCTTCCAAACACTGTTATTTGGTAAAGTAACAATATACCTTCCAGT 3840  
Db 3781 AAGAGCTTCCTGCTTCCAAACACTGTTATTTGGTAAAGTAACAATATACCTTCCAGT 3840  
OY 3841 CTACTAGGATAGCAGCCGTTGCTACCGAGTGTGTCTTAAGAACACAGAGAGAAATTA 3900  
Db 3841 CTACTAGGATAGCAGCCGTTGCTACCGAGTGTGTCTTAAGAACACAGAGAGAAATTA 3900  
OY 3901 TATCATTTGAAGATAGCTTAATGAGTGCAGTAACCAAGGTAATTTGGCAAGGCAATC 3960  
Db 3901 TATCATTTGAAGATAGCTTAATGAGTGCAGTAACCAAGGTAATTTGGCAAGGCAATC 3960  
OY 3961 AGGACATACCTTAAGTGAAGAAACAAATGTTCTGCTAGCTTGTTCCTACAGTGA 4020  
Db 3961 AGGACATACCTTAAGTGAAGAAACAAATGTTCTGCTAGCTTGTTCCTACAGTGA 4020  
OY 4021 GTGAATTTGAAGCTGATGCAATTAACAACCAAGATCCTTTCTTGATGTTGTTCTT 4080  
Db 4021 GTGAATTTGAAGCTGATGCAATTAACAACCAAGATCCTTTCTTGATGTTGTTCTT 4080  
OY 4081 CCAAAACAAATGAAGCATAGTGTGAAGAGCCAGAGATTTGGTGTGATGCAAGGAATGG 4140  
Db 4081 CCAAAACAAATGAAGCATAGTGTGAAGAGCCAGAGATTTGGTGTGATGCAAGGAATGG 4140

---

OY 4141 TTTCAGATGATGAAGAAAGAGACGGGCTTGGAAGAAAAATATCAAGAGCAAGACA 4200  
Db 4141 TTTCAGATGATGAAGAAAGAGACGGGCTTGGAAGAAAAATATCAAGAGCAAGACA 4200  
OY 4201 TGGATTCAAACTTAGTGAAGACGATCTGGGTGTGAGAGTGAACACGCTCTGGAAG 4260  
Db 4201 TGGATTCAAACTTAGTGAAGACGATCTGGGTGTGAGAGTGAACACGCTCTGGAAG 4260  
OY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAAACCTCAGCAGAGGATACATGC 4320  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAAACCTCAGCAGAGGATACATGC 4320  
OY 4321 AACATACCTGATTAAGCTCCAGCAGAGAAATGGCTGAAGTGTGTTAAGAACAC 4380  
Db 4321 AACATACCTGATTAAGCTCCAGCAGAGAAATGGCTGAAGTGTGTTAAGAACAC 4380  
OY 4381 ATGGAGCCAGCCTTTAAGCAGCTACCTTCATCTAAGTGAATCTTCTGCCCTTGAG 4440  
Db 4381 ATGGAGCCAGCCTTTAAGCAGCTACCTTCATCTAAGTGAATCTTCTGCCCTTGAG 4440  
OY 4441 ACCTGCAATCCAGAACAAAGACATCAGAAAAGCAGTATTAACCTCAGAGAAAATG 4500  
Db 4441 ACCTGCAATCCAGAACAAAGACATCAGAAAAGCAGTATTAACCTCAGAGAAAATG 4500  
OY 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGCAAGTGTGAGTGTG 4560  
Db 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGCAAGTGTGAGTGTG 4560  
OY 4561 CAGATAGTTCACAGTAAAAATTAAGAACAGAGTGAAGATATCCCTTCTTAAT 4620  
Db 4561 CAGATAGTTCACAGTAAAAATTAAGAACAGAGTGAAGATATCCCTTCTTAAT 4620  
OY 4621 GCCATCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
Db 4621 GCCATCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
OY 4681 ACTACCATCTCAGAGAGCTCATTAAGTGTGTGATGATGATGATGATGATGATGATG 4740  
Db 4681 ACTACCATCTCAGAGAGCTCATTAAGTGTGTGATGATGATGATGATGATGATGATG 4740  
OY 4741 AGTCTGGGCAACGATTTGACAGGAAACATCTTACTGCGCAAGGCAAGATCTAGAGGGA 4800  
Db 4741 AGTCTGGGCAACGATTTGACAGGAAACATCTTACTGCGCAAGGCAAGATCTAGAGGGA 4800  
OY 4801 CCCCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4860  
Db 4801 CCCCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4860  
OY 4861 AAGACAGAGCCCGAGAGTCAAGTCTGTTGGCAACATACCATCTTCACCTGATGA 4920  
Db 4861 AAGACAGAGCCCGAGAGTCAAGTCTGTTGGCAACATACCATCTTCACCTGATGA 4920  
OY 4921 AAGTTCCTCAATTTGAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980  
Db 4921 AAGTTCCTCAATTTGAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980  
OY 4981 ATATCTGCTGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
Db 4981 ATATCTGCTGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
OY 5041 CTTCAACAGAAAGGGTCAACAAAGATGTCATGGTGTCTGGCTGACCCCGAAG 5100  
Db 5041 CTTCAACAGAAAGGGTCAACAAAGATGTCATGGTGTCTGGCTGACCCCGAAG 5100  
OY 5101 AATTTATGCTGCTGTAACAAGTTTGCAGAAAACACACATCTTAATCTAATTA 5160  
Db 5101 AATTTATGCTGCTGTAACAAGTTTGCAGAAAACACACATCTTAATCTAATTA 5160  
OY 5161 CTGAAGAGACTACTATGTTGTTATGAAGAAACAGATGATGATGATGATGATGATGATG 5220  
Db 5161 CTGAAGAGACTACTATGTTGTTATGAAGAAACAGATGATGATGATGATGATGATGATG 5220



OY 5221 TGAATATTTTCTAGGAATTCGGGAGCAAAATGGTAGTTAGTATTTCTGGGTGACC 5280  
|||||  
DB 5221 TGAATATTTTCTAGGAATTCGGGAGCAAAATGGTAGTTAGTATTTCTGGGTGACC 5280  
OY 5281 AGCTCTTTAAGAAAGAAAATGCTGAATAGCATGATTTTGAAGTACAGAGAGATGTGG 5340  
|||||  
DB 5281 AGCTCTTTAAGAAAGAAAATGCTGAATAGCATGATTTTGAAGTACAGAGAGATGTGG 5340  
OY 5341 TCAATGGAAGAAACACACAGGTCCAAAGCGAGCAGAGATCCAGACAGAAAGATCT 5400  
|||||  
DB 5341 TCAATGGAAGAAACACACAGGTCCAAAGCGAGCAGAGATCCAGACAGAAAGATCT 5400  
OY 5401 TCAGGGGGCTAGAAATCTGTCTATAGGGCCCTTACCAACATGCCACAGATTAAGTGG 5460  
|||||  
DB 5401 TCAGGGGGCTAGAAATCTGTCTATAGGGCCCTTACCAACATGCCACAGATTAAGTGG 5460  
OY 5461 AATGATGTGACAGCTGTGTGTGCTCTGTGTGAAGAGACTTTCATCTACCTTG 5520  
|||||  
DB 5461 AATGATGTGACAGCTGTGTGTGCTCTGTGTGAAGAGACTTTCATCTACCTTG 5520  
OY 5521 GCACAGGTGTCACCCAAATGTGTGTGTGACAGCCAGATGCCGTGACAGAGACAATGGCT 5580  
|||||  
DB 5521 GCACAGGTGTCACCCAAATGTGTGTGTGACAGCCAGATGCCGTGACAGAGACAATGGCT 5580  
OY 5581 TCCATGCAATTTGGGAGATGTGTAGGACAGCTGTGTGACCCAGAGATGGGTGTGGACA 5640  
|||||  
DB 5581 TCCATGCAATTTGGGAGATGTGTAGGACAGCTGTGTGACCCAGAGATGGGTGTGGACA 5640  
OY 5641 GTGTAGCACTCTACAGTGGCAGAGCTGGACACCTACCTGATACCCAGATCCCCACA 5700  
|||||  
DB 5641 GTGTAGCACTCTACAGTGGCAGAGCTGGACACCTACCTGATACCCAGATCCCCACA 5700  
OY 5701 GCCACTACTGA 5711  
|||||  
DB 5701 GCCACTACTGA 5711  
RESULT 14  
LOCUS 140803 5712 bp DNA PAT 01-MAY-1997  
DEFINITION Sequence 12 from patent US 5622829.  
ACCESSION 140803  
NID 92082283  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5712)  
AUTHORS King, M., Friedmann, L., Ostermeyer, B., Rowell, S., Lynch, E., Szabo, C.  
and Lee, M.  
TITLE Genetic markers for breast, ovarian, and prostatic cancer  
JOURNAL Patent: US 5622829-A 12 22-APR-1997;  
FEATURES Location/Qualifiers  
source 1..5712  
BASE COUNT 1957 a 1099 c 1274 g 1382 t  
ORIGIN  
Query Match 99.8%; Score 5698.4; DB 6; Length 5712;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

DB 121 TGAATTTATCTGCTCTTCGGCTGAAGAGTACAAAATGCTATTATGCTATGACGAAAA 180  
OY 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACCTGTCTCCACAAAGTGTACC 240  
|||||  
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACCTGTCTCCACAAAGTGTACC 240  
OY 241 ACATATTTTGCATAATTTGATGCTGAACCTCTCAACGAGAAAGAGGCGCTTACAGT 300  
|||||  
DB 241 ACATATTTTGCATAATTTGATGCTGAACCTCTCAACGAGAAAGAGGCGCTTACAGT 300  
OY 301 GTCCCTTATGTAAGATGATATACCAAGAGAGCTTACAGAAAGATGAGATTTAGTC 360  
|||||  
DB 301 GTCCCTTATGTAAGATGATATACCAAGAGAGCTTACAGAAAGATGAGATTTAGTC 360  
OY 361 AACTGTTGAAGAGCTATTGAAAATCATTTGTCTTTGAGCTTGACACAGGTTTGGAGT 420  
|||||  
DB 361 AACTGTTGAAGAGCTATTGAAAATCATTTGTCTTTGAGCTTGACACAGGTTTGGAGT 420  
OY 421 ATGCAAAAGCTATATTTTGCAAAAGAAATTAACCTGCTGAACATCTAAAAAGATG 480  
|||||  
DB 421 ATGCAAAAGCTATATTTTGCAAAAGAAATTAACCTGCTGAACATCTAAAAAGATG 480  
OY 481 AAGTTCTATCATCAAAAGTATGGCTTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
|||||  
DB 481 AAGTTCTATCATCAAAAGTATGGCTTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
OY 541 AACCCGAAAATCTCTCTTGCAGGAAACCAAGTCTCAGTCCAACTCTTAACTTGGAA 600  
|||||  
DB 541 AACCCGAAAATCTCTCTTGCAGGAAACCAAGTCTCAGTCCAACTCTTAACTTGGAA 600  
OY 601 CTGTGGAACCTCTGAGAACAAAGCAGCGATCAACCTGAAAAGAGTGTCTACATTG 660  
|||||  
DB 601 CTGTGGAACCTCTGAGAACAAAGCAGCGATCAACCTGAAAAGAGTGTCTACATTG 660  
OY 661 AATTGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCACTTATGCACTGTGGAG 720  
|||||  
DB 661 AATTGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCACTTATGCACTGTGGAG 720  
OY 721 ATCAAGAAATTTGTAACAATCACCCCTCAAGGAACCAAGGATTAATCTAGTTTGTG 780  
|||||  
DB 721 ATCAAGAAATTTGTAACAATCACCCCTCAAGGAACCAAGGATTAATCTAGTTTGTG 780  
OY 781 CAAAAAAGGCTGTGTGAATTTCTGAGAGGATGTAACAATCTGACATCATCAAC 840  
|||||  
DB 781 CAAAAAAGGCTGTGTGAATTTCTGAGAGGATGTAACAATCTGACATCATCAAC 840  
OY 841 CCAGTAATATGATTTGAACACACCTGAGAACGCTGACAGCTGAGAGCATCCAGAAAAGT 900  
|||||  
DB 841 CCAGTAATATGATTTGAACACACCTGAGAACGCTGACAGCTGAGAGCATCCAGAAAAGT 900  
OY 901 ATCAGGCTGATCTGTTTAAACTTGACATGTGAGCATGTGGCAAAATACTATGCCA 960  
|||||  
DB 901 ATCAGGCTGATCTGTTTAAACTTGACATGTGAGCATGTGGCAAAATACTATGCCA 960  
OY 961 GCTCATTACAGATGAGAACAGAGATTTTACTACATTAAGACAGAAATGATGTAGAAA 1020  
|||||  
DB 961 GCTCATTACAGATGAGAACAGAGATTTTACTACATTAAGACAGAAATGATGTAGAAA 1020  
OY 1021 AGGCTGAATTTCTGTAATAAAGCAACACCTGCTGTAGCAAGAGCCACATTAACAGAT 1080  
|||||  
DB 1021 AGGCTGAATTTCTGTAATAAAGCAACACCTGCTGTAGCAAGAGCCACATTAACAGAT 1080  
OY 1081 GGGCTGGAAGTAAGAAACATGTAATGATAGCGGATCCACGACACAGAAAAAGGTAG 1140  
|||||  
DB 1081 GGGCTGGAAGTAAGAAACATGTAATGATAGCGGATCCACGACACAGAAAAAGGTAG 1140  
OY 1141 ATCTGATGCTGATCCCTGCTGTGAGAGAAAGATGGAATTAAGCAAAATGCAATGCT 1200  
|||||  
DB 1141 ATCTGATGCTGATCCCTGCTGTGAGAGAAAGATGGAATTAAGCAAAATGCAATGCT 1200  
OY 1201 CAGAGATCTCTAGATATCTGAAGATGTTCTTGTGATTAACCTAATATGACGATTCAGA 1260  
|||||  
DB 1201 CAGAGATCTCTAGATATCTGAAGATGTTCTTGTGATTAACCTAATATGACGATTCAGA 1260



QY 1261 AAGTATAGATGTTTCCAGAAAGTATGATGACTGTAGTTCGTATGACTACATGATG 1320  
DB 1261 AAGTATAGATGTTTCCAGAAAGTATGATGACTGTAGTTCGTATGACTACATGATG 1320  
QY 1321 GGGAGTGTGATCAATCAAGTACGTATGATGAGAGTTCCTAAATGAGGTAGTG 1380  
DB 1321 GGGAGTGTGATCAATCAAGTACGTATGATGAGAGTTCCTAAATGAGGTAGTG 1380  
QY 1381 AATATTCGTCTTCAGAGAAATAGACTTACTGGCCAGTATCTCATGAGGCTTTAA 1440  
DB 1381 AATATTCGTCTTCAGAGAAATAGACTTACTGGCCAGTATCTCATGAGGCTTTAA 1440  
QY 1441 TAGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATATATTTGAAGACAAAATAT 1500  
DB 1441 TAGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATATATTTGAAGACAAAATAT 1500  
QY 1501 TTGGGAAACCTATCGGAGAGAGGCAAGCCCTCCCAACTTAAGCCATGTAAGTAAATC 1560  
DB 1501 TTGGGAAACCTATCGGAGAGAGGCAAGCCCTCCCAACTTAAGCCATGTAAGTAAATC 1560  
QY 1561 TAATATAGAGAGATTTGTACTGAGCCACAGATATATACAGAGCCTCCCTCACAATA 1620  
DB 1561 TAATATAGAGAGATTTGTACTGAGCCACAGATATATACAGAGCCTCCCTCACAATA 1620  
QY 1621 AATTTAAAGCTAAAAGAGACCTTACATCAGGCCCTTCCTCAGAGATTTATCAAGAAAG 1680  
DB 1621 AATTTAAAGCTAAAAGAGACCTTACATCAGGCCCTTCCTCAGAGATTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGAGTTCAAAAGAGACCTCTGAATATGATATCAGGGAACTTAACCAAGGAGC 1740  
DB 1681 CAGATTTGGAGTTCAAAAGAGACCTCTGAATATGATATCAGGGAACTTAACCAAGGAGC 1740  
QY 1741 AGATGCTCAAGTATGATGATATTAATAGTGTCTATGAGATTAATTAAGAAAGGTATT 1800  
DB 1741 AGATGCTCAAGTATGATGATATTAATAGTGTCTATGAGATTAATTAAGAAAGGTATT 1800  
QY 1801 CTATTCGAGATGAGAAAAATCTTAACCATAGATATCCTCGAAAAAGAAATCTGCTTTCA 1860  
DB 1801 CTATTCGAGATGAGAAAAATCTTAACCATAGATATCCTCGAAAAAGAAATCTGCTTTCA 1860  
QY 1861 AAAGAAAGCTGAACCTATATAGAGAGAGTATTAAGCAATATGAACTGAATTAATATTC 1920  
DB 1861 AAAGAAAGCTGAACCTATATAGAGAGAGTATTAAGCAATATGAACTGAATTAATATTC 1920  
QY 1921 ACAATTCAAAAGACCTTAATAAGATAGGCTGAAGAGAGTCTTCTACAGAGCATATTC 1980  
DB 1921 ACAATTCAAAAGACCTTAATAAGATAGGCTGAAGAGAGTCTTCTACAGAGCATATTC 1980  
QY 1981 ATGCGCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
DB 1981 ATGCGCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
QY 2041 TTGATATGTTGTCTAGAGTGAAGAGATTAAGAAAGTAAAGTAAAGTAAAGTAAAGTAA 2100  
DB 2041 TTGATATGTTGTCTAGAGTGAAGAGATTAAGAAAGTAAAGTAAAGTAAAGTAAAGTAA 2100  
QY 2101 GGCAGACAGAAAACCTTCAACTCATGAGAGTAAAGAACTGCAACTGAGAGCCAAAGAGA 2160  
DB 2101 GGCAGACAGAAAACCTTCAACTCATGAGAGTAAAGAACTGCAACTGAGAGCCAAAGAGA 2160  
QY 2161 GTAAACAGGCCAATGAACACAGTAAAGAGACATGACAGCACTTCTCCAGAGCTGA 2220  
DB 2161 GTAAACAGGCCAATGAACACAGTAAAGAGACATGACAGCACTTCTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAAATGACCTGCTCTTTTACTAAGTTCATTAATACAGAGATTAAGAAAT 2280  
DB 2221 AGTTAAACAAATGACCTGCTCTTTTACTAAGTTCATTAATACAGAGATTAAGAAAT 2280  
QY 2281 TTGTCATCTAGCCTTCCAG 2340  
DB 2281 TTGTCATCTAGCCTTCCAG 2340

QY 2341 CTAATAATGCTGAAGAGCCCAAGATCTCATGTTAGTGAGAGAGAGGCTTTGCAAACTG 2400  
DB 2341 CTAATAATGCTGAAGAGCCCAAGATCTCATGTTAGTGAGAGAGAGGCTTTGCAAACTG 2400  
QY 2401 AAAGATCTGAGAGAGTACGATATTTTCACTGTTAGTACGTATGATGATGATGATGATG 2460  
DB 2401 AAAGATCTGAGAGAGTACGATATTTTCACTGTTAGTACGTATGATGATGATGATGATG 2460  
QY 2461 AAGATATCTGCTTACTGGAAGTATGACCTCTAGGGAAGGCAAAAAGCAAAATTAAT 2520  
DB 2461 AAGATATCTGCTTACTGGAAGTATGACCTCTAGGGAAGGCAAAAAGCAAAATTAAT 2520  
QY 2521 GTGTGATCAGTGTGACAGCTTTGAAAACCCCAAGGAGCAATTAATGATGTTTCCAAAG 2580  
DB 2521 GTGTGATCAGTGTGACAGCTTTGAAAACCCCAAGGAGCAATTAATGATGTTTCCAAAG 2580  
QY 2581 ATATATGAAATGACACAGAGGCTTTAAGTATCATTTGGAGATGAAATTAACACAGTC 2640  
DB 2581 ATATATGAAATGACACAGAGGCTTTAAGTATCATTTGGAGATGAAATTAACACAGTC 2640  
QY 2641 GGGAAACAAACATAGAAATGGAAGAAAGTGAAGTATGCTCAGATATTTGCAATATCAT 2700  
DB 2641 GGGAAACAAACATAGAAATGGAAGAAAGTGAAGTATGCTCAGATATTTGCAATATCAT 2700  
QY 2701 TCAAGGTTTCAAGGCGCAGATCTTTGCTGTTTCAATCCAGAGAAATGCAAGAGAG 2760  
DB 2701 TCAAGGTTTCAAGGCGCAGATCTTTGCTGTTTCAATCCAGAGAAAGTGAAGAGAG 2760  
QY 2761 AATGTCACATTTCTGCCCACATCTGCTGCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
DB 2761 AATGTCACATTTCTGCCCACATCTGCTGCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGAGAAATCAAGAAAGTGAAGTATATATCAAGCTGTAC 2880  
DB 2821 TTGAATGTGAACAAAGAGAAATCAAGAAAGTGAAGTATATATCAAGCTGTAC 2880  
QY 2881 AGACAGTATATATCTGAGGCTTCTGCTGTTGCTGAGAAAGATTAACAGCTGATATA 2940  
DB 2881 AGACAGTATATATCTGAGGCTTCTGCTGTTGCTGAGAAAGATTAACAGCTGATATA 2940  
QY 2941 ATGCAAAATGATATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
DB 2941 ATGCAAAATGATATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
QY 3001 ACAGAACTGAGCTATTAATCAAAATTAACATGAGCTTTTACAAACCCATATCTATAC 3060  
DB 3001 ACAGAACTGAGCTATTAATCAAAATTAACATGAGCTTTTACAAACCCATATCTATAC 3060  
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTTAAACCTAATGTAAGAAATCTGCTAGAGG 3120  
DB 3061 CACCACTTTTCCCATCAAGTCAATTTGTTTAAACCTAATGTAAGAAATCTGCTAGAGG 3120  
QY 3121 AAAAATTTGAGAAACATCAATGACCTGAAGAGAGAAAGGAGAAATGAGAAATTCGAA 3180  
DB 3121 AAAAATTTGAGAAACATCAATGACCTGAAGAGAGAAAGGAGAAATGAGAAATTCGAA 3180  
QY 3181 GTACAGTGAACCAATTAAGCTTAATTAACATTAAGAGAAATGTTTAAAGAGCCAGCT 3240  
DB 3181 GTACAGTGAACCAATTAAGCTTAATTAACATTAAGAGAAATGTTTAAAGAGCCAGCT 3240  
QY 3241 CAAGCAATTAATTAAGAGTGTGCTCAAGTCTATGAGAGGCTCCAGATTAATGAA 3300  
DB 3241 CAAGCAATTAATTAAGAGTGTGCTCAAGTCTATGAGAGGCTCCAGATTAATGAA 3300  
QY 3301 TAGGTTCCAGTGAAGAAACATCAAGCAGAGTATAGTAAACAGAGGCCCAAAATGGA 3360  
DB 3301 TAGGTTCCAGTGAAGAAACATCAAGCAGAGTATAGTAAACAGAGGCCCAAAATGGA 3360  
QY 3361 ATGCTATGCTTAGATTAAGGAGTTTGCACACCTGAGGCTATTAACAAAGTCTCTGGA 3420  
DB 3361 ATGCTATGCTTAGATTAAGGAGTTTGCACACCTGAGGCTATTAACAAAGTCTCTGGA 3420  
QY 3421 GTAAATGTGAAGCATCTGAAATTAAGAAAGCAGAGATATGAAGAGTATGAGTTCAGATGTTA 3480

```
Db 3421 GTAAATGTAAGCATCCGTAATAAAGCAAGATATGAAGAAAGTAAGTACTGTTA 3480
Oy 3481 ATACAGATTTCTCTCCATATCTGATTTAGATAACTTGAACAGCCTTGGGAAGTACTC 3540
Db 3481 ATACAGATTTCTCTCCATATCTGATTTAGATAACTTGAACAGCCTTGGGAAGTACTC 3540
Oy 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTGATGATGATGTTAAATAAAG 3600
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTGATGATGATGTTAAATAAAG 3600
Oy 3601 AAGATACTAGTTTGTGTAATAATGACATTAAGAAAGTTCAGTTTGAACAAAGCG 3660
Db 3601 AAGATACTAGTTTGTGTAATAATGACATTAAGAAAGTTCAGTTTGAACAAAGCG 3660
Oy 3661 TCCAGAAAGAGAGACTTAGCAGAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAG 3720
Db 3661 TCCAGAAAGAGAGACTTAGCAGAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAG 3720
Oy 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAAGAGACTTATCTAGTGAGATG 3780
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAAGAGACTTATCTAGTGAGATG 3780
Oy 3781 AAGAGCTTCCCTGCTCCACACTTGTATTGTTAAAGTAAAGCAATATACCTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTCCACACTTGTATTGTTAAAGTAAAGCAATATACCTCTCAGT 3840
Oy 3841 CTACTAGGCATAGCACCGTGTCTACCGAGTGTCTGTAGAACACAGAGAGAGATTTAT 3900
Db 3841 CTACTAGGCATAGCACCGTGTCTACCGAGTGTCTGTAGAACACAGAGAGAGATTTAT 3900
Oy 3901 TATCATGTAAGATAGCTTAAATGATACAGTACACAGTAATTTGGCAAGAGCATCTC 3960
Db 3901 TATCATGTAAGATAGCTTAAATGATACAGTACACAGTAATTTGGCAAGAGCATCTC 3960
Oy 3961 AGGACATCACTTGTAGTGAAGAAACAAATGTTCTGCTAGCTTCTTCTCAGAGTGA 4020
Db 3961 AGGACATCACTTGTAGTGAAGAAACAAATGTTCTGCTAGCTTCTTCTCAGAGTGA 4020
Oy 4021 GTGAATTTGGAAGACTTGACCTGCAAAATACAAACCCAGAGATCTTCTGTGATTTGTT 4080
Db 4021 GTGAATTTGGAAGACTTGACCTGCAAAATACAAACCCAGAGATCTTCTGTGATTTGTT 4080
Oy 4081 CCAAAATAATGAGCATCACTGTAAGCCAGGAGTGTGCTAGTGAAGCAAGAAATTTG 4140
Db 4081 CCAAAATAATGAGCATCACTGTAAGCCAGGAGTGTGCTAGTGAAGCAAGAAATTTG 4140
Oy 4141 TTTGAGATGATGAAGAAAGAGAAAGGCTTGGAAAGAAATTAATCAAGAAAGCAAGCA 4200
Db 4141 TTTGAGATGATGAAGAAAGAGAAAGGCTTGGAAAGAAATTAATCAAGAAAGCAAGCA 4200
Oy 4201 TGGATTCAAACTTAAAGTGAAGCAGCATCTGGGTGTGAGAGTGAAGCAAGCGTCTGAG 4260
Db 4201 TGGATTCAAACTTAAAGTGAAGCAGCATCTGGGTGTGAGAGTGAAGCAAGCGTCTGAG 4260
Oy 4261 ACTGCTCAGGGGCTATCTCTCAGAGTGAATTTTAACCATCTCAGCAGAGGATACCATGC 4320
Db 4261 ACTGCTCAGGGGCTATCTCTCAGAGTGAATTTTAACCATCTCAGCAGAGGATACCATGC 4320
Oy 4321 AACATTAACCTGATTAAGAGTCCAGAGAAATGGCTGAATAGAAAGTGTGTAGAAAGC 4380
Db 4321 AACATTAACCTGATTAAGAGTCCAGAGAAATGGCTGAATAGAAAGTGTGTAGAAAGC 4380
Oy 4381 ATGGAGGCCAGCCTTTAAACAGTACCTTCCATCATTAAGTGAATCTTGTGCCCTTGG 4440
Db 4381 ATGGAGGCCAGCCTTTAAACAGTACCTTCCATCATTAAGTGAATCTTGTGCCCTTGG 4440
Oy 4441 ACCTGGAAATCCAGAAAGCAGACATCAGAAAGAGAGATTAATCACTTCAAGAAAGTA 4500
Db 4441 ACCTGGAAATCCAGAAAGCAGACATCAGAAAGAGAGATTAATCACTTCAAGAAAGTA 4500
Oy 4501 GTGAATACCTTAAAGCCAGAAATCAGAAAGGCTTCTGCTGACAAAGTGTGAGTGTG 4560
Db 4501 GTGAATACCTTAAAGCCAGAAATCAGAAAGGCTTCTGCTGACAAAGTGTGAGTGTG 4560
```

```
Db 4501 GTGAATACCTTAAAGCCAGAAATCAGAAAGGCTTCTGCTGACAAAGTGTGAGTGTG 4560
Oy 4561 CAGATAGTTCACAGTAAATAAAGAACAGAGTGAAGAGTATCCCTTTCTTAAT 4620
Db 4561 CAGATAGTTCACAGTAAATAAAGAACAGAGTGAAGAGTATCCCTTTCTTAAT 4620
Oy 4621 GCCCATCATTTAGATAGTGTGTACATGCACAGTGTCTGTGGAGTCTTCAGATAGAA 4680
Db 4621 GCCCATCATTTAGATAGTGTGTGTACATGCACAGTGTCTGTGGAGTCTTCAGATAGAA 4680
Oy 4681 ACTACCATCTCAAGAGAGCTCATTAAGTGTGTAGTGTGAGAGAGCAACAGCTGGAAG 4740
Db 4681 ACTACCATCTCAAGAGAGCTCATTAAGTGTGTAGTGTGAGAGAGCAACAGCTGGAAG 4740
Oy 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCCAAAGCAAGATCTAGAGGAA 4800
Db 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCCAAAGCAAGATCTAGAGGAA 4800
Oy 4801 CCCCTTACCTGGAAATCTGGAATCAGCCTCTTCTGTGATGACCTGAATCTGATCTTCTG 4860
Db 4801 CCCCTTACCTGGAAATCTGGAATCAGCCTCTTCTGTGATGACCTGAATCTGATCTTCTG 4860
Oy 4861 AAGACAGAGCCAGAGTCAAGTCTGTTGGCAACATACCATCTCAACCTGCACTTGA 4920
Db 4861 AAGACAGAGCCAGAGTCAAGTCTGTTGGCAACATACCATCTCAACCTGCACTTGA 4920
Oy 4921 AAGTTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTGCTACTACTG 4980
Db 4921 AAGTTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTGCTACTACTG 4980
Oy 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGAGGAGAAAGCCAGATTCAG 5040
Db 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGAGGAGAAAGCCAGATTCAG 5040
Oy 5041 CTTCAACAGAAAGAGTCAACAAAGAAATGTCATGGTGTGCTGAGCTGAGCCAGAG 5100
Db 5041 CTTCAACAGAAAGAGTCAACAAAGAAATGTCATGGTGTGCTGAGCTGAGCCAGAG 5100
Oy 5101 AATTTATGCTGTGTACAGATTTGCCAGAAACACACATCACTTAATCTAATTA 5160
Db 5101 AATTTATGCTGTGTACAGATTTGCCAGAAACACACATCACTTAATCTAATTA 5160
Oy 5161 CTGAAGAGTACTCATGTTGTTATGAAGAAACAGATCTGATGTTGTGTGAACGAGAC 5220
Db 5161 CTGAAGAGTACTCATGTTGTTATGAAGAAACAGATCTGATGTTGTGTGAACGAGAC 5220
Oy 5221 TGAATATTTTCTAGGAATTTGCGGAGAGAAATGGTATGATCTTCTGCTGGTGACCC 5280
Db 5221 TGAATATTTTCTAGGAATTTGCGGAGAGAAATGGTATGATCTTCTGCTGGTGACCC 5280
Oy 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATG 5340
Db 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATG 5340
Oy 5341 TCAATGGAAGAAACCAAGGTCGCAAGGTCGCAAGGTCGCAAGGTCGCAAGGTCGCAAG 5400
Db 5341 TCAATGGAAGAAACCAAGGTCGCAAGGTCGCAAGGTCGCAAGGTCGCAAGGTCGCAAG 5400
Oy 5401 TCAAGGGGCTAGAAATCTGTGCTATAGGGCCCTTCAACCAATGCCCAGATCAACTGG 5460
Db 5401 TCAAGGGGCTAGAAATCTGTGCTATAGGGCCCTTCAACCAATGCCCAGATCAACTGG 5460
Oy 5461 AATGATGTTGACAGCTGTGTGTCTGTGTGTGAAGAGCTTTCATCATTCACCTTGG 5520
Db 5461 AATGATGTTGACAGCTGTGTGTCTGTGTGTGAAGAGCTTTCATCATTCACCTTGG 5520
Oy 5521 GCACAGTGTCCACCAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5580
Db 5521 GCACAGTGTCCACCAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5580
Oy 5581 TCCATGCAATTTGGGAGATGTGTGAAGCAGCTGTGTGTGACCCGAGAGTGTGTGTGTG 5640
Db 5581 TCCATGCAATTTGGGAGATGTGTGAAGCAGCTGTGTGTGACCCGAGAGTGTGTGTGTG 5640
```

Query 5641 GGTAGACTCTACACAGGAGAGAGCTGAGACCT-ACCTGATACCCAGATCCCCAC 5699  
Db 5641 GGTAGACTCTACACAGGAGAGCTGAGACCTACCTGATACCCAGATCCCCAC 5700  
QY 5700 AGCCACTACTGA 5711  
Db 5701 AGCCACTACTGA 5712

RESULT 15  
LOCUS 140797 5710 bp DNA PAT 01-MAY-1997  
DEFINITION Sequence 6 from patent US 5622829.  
ACCESSION 140797  
NID 92082277  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5710)  
AUTHORS King, M., Friedman, L., Ostermeyer, B., Rowell, S., Lynch, E., Szabo, C.  
and Lee, M.  
TITLE Genetic markers for breast, ovarian, and prostatic cancer  
JOURNAL Patent: US 5622829-A 6 22-Apr-1997;  
FEATURES  
source 1..5710  
1..5710  
BASE COUNT 1955 a 1099 c 1274 g 1382 t  
ORIGIN

Query Match 99.8%; Score 5697.4; DB 6; Length 5710;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5709; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AGCTGCTGAGACTTCTCTGAGACCCGACAGGCTGTGGGTTTCTCAATACCTGGCC 60  
Db 1 AGCTGCTGAGACTTCTCTGAGACCCGACAGGCTGTGGGTTTCTCAATACCTGGCC 60  
QY 61 CCGGCGCTGAGAGGCGCTTACCCCTGCTGGGTGAAGTTTCATTTGGAACGAAAGAA 120  
Db 61 CCGGCGCTGAGAGGCGCTTACCCCTGCTGGGTGAAGTTTCATTTGGAACGAAAGAA 120  
QY 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCTTAATGCTATGCAAAAA 180  
Db 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCTTAATGCTATGCAAAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTTGATCAAGAACCTGTCTCACAAGGTGACC 240  
Db 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTTGATCAAGAACCTGTCTCACAAGGTGACC 240  
QY 241 ACATATTTTGAATTTTGCATGCTGAACCTTCTCAACAGAAAGAGGCGCTTCACAGT 300  
Db 241 ACATATTTTGAATTTTGCATGCTGAACCTTCTCAACAGAAAGAGGCGCTTCACAGT 300  
QY 301 GTCCCTTATGAAGATGATATTAACCAAGAGAGCTTACAGAAAGTACGAGATTAGTC 360  
Db 301 GTCCCTTATGAAGATGATATTAACCAAGAGAGCTTACAGAAAGTACGAGATTAGTC 360  
QY 361 AACTTGTGAAGAGCTATTTGAAATATTTTGTCTTTCAAGCTTGACACAGGTTTGAAT 420  
Db 361 AACTTGTGAAGAGCTATTTGAAATATTTTGTCTTTCAAGCTTGACACAGGTTTGAAT 420  
QY 421 ATGCAAGAGCTATTTTGAAGAAATTAATCTCTCTGAAACATCTTAAAGATG 480  
Db 421 ATGCAAGAGCTATTTTGAAGAAATTAATCTCTCTGAAACATCTTAAAGATG 480  
QY 481 AAGTTTCTATCATCAAGATAGGGCTACAGAAACCGTGCAAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCAAGATAGGGCTACAGAAACCGTGCAAAAGACTTCTACAGAGTG 540  
QY 541 AACCGAAATCTCTCTTGGAGGAAACAGTCTCACTGCTCACTTACCTTGGAA 600

Db 541 AACCGAAATCTCTCTTGGAGGAAACAGTCTCACTGCTCACTTACCTTGGAA 600  
QY 601 CTGTGAGAACTCTGAGAGCAAGAGCGGATACAACTCAAAAGAGCTGTCTACATG 660  
Db 601 CTGTGAGAACTCTGAGAGCAAGAGCGGATACAACTCAAAAGAGCTGTCTACATG 660  
QY 661 AATGGGATCTGATCTTCTGAGATACCGTTAATTAAGCAACTTAATGCACTGAGAG 720  
Db 661 AATGGGATCTGATCTTCTGAGATACCGTTAATTAAGCAACTTAATGCACTGAGAG 720  
QY 721 ATCAAGAAATGTTTACAAATCAACCCCTCAAGAGCAAGGATGAATTCGATTCG 780  
Db 721 ATCAAGAAATGTTTACAAATCAACCCCTCAAGAGCAAGGATGAATTCGATTCG 780  
QY 781 CAAAAAGAGCTCTGTTGTAATTTCTGAGAGCGGATGTAACAATCTGAAATCATCAAC 840  
Db 781 CAAAAAGAGCTCTGTTGTAATTTCTGAGAGCGGATGTAACAATCTGAAATCATCAAC 840  
QY 841 CCAGTATATGATTTGAACACCACTGAGAGCGGTGACCTGAGAGGATCCAGAAAGT 900  
Db 841 CCAGTATATGATTTGAACACCACTGAGAGCGGTGACCTGAGAGGATCCAGAAAGT 900  
QY 901 ATCAGGATGCTCTGTTTCAACTGCAATGTGAGCCATGTGGCAAAATACTACATGCA 960  
Db 901 ATCAGGATGCTCTGTTTCAACTGCAATGTGAGCCATGTGGCAAAATACTACATGCA 960  
QY 961 GCTCATTAAGCATGAGAACACAGCTTTTATCTCACTAATAAGCAAGATGTAAGAA 1020  
Db 961 GCTCATTAAGCATGAGAACACAGCTTTTATCTCACTAATAAGCAAGATGTAAGAA 1020  
QY 1021 AGGCTGAATCTGTAATTAAGCAAGAGCTGCTTACCAAGAGCCACATTAACAGAT 1080  
Db 1021 AGGCTGAATCTGTAATTAAGCAAGAGCTGCTTACCAAGAGCCACATTAACAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGAGGCGGACCTCCGACAGAAAGAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGAGGCGGACCTCCGACAGAAAGAGGTAG 1140  
QY 1141 ATCTGAATCTGATCCCTGCTGTGAGAGAAAGAAATGAAATAGCAGAAACTGCCATG 1200  
Db 1141 ATCTGAATCTGATCCCTGCTGTGAGAGAAAGAAATGAAATAGCAGAAACTGCCATG 1200  
QY 1201 CAGAGATCTTGAAGATGATGATGTTCTTGGATTAACCTAATATACAGATTCAGA 1260  
Db 1201 CAGAGATCTTGAAGATGATGATGTTCTTGGATTAACCTAATATACAGATTCAGA 1260  
QY 1260 AAGTTAATGAGTGTTCCTCAAGAGATGATGATGTTCTGATGATGATGATGATG 1320  
Db 1260 AAGTTAATGAGTGTTCCTCAAGAGATGATGATGTTCTGATGATGATGATGATG 1320  
QY 1321 GGGAGCTGAATCAATGCAAGAGTGTGATGATGTTTGGAGCTTCAATATGAGATGATG 1380  
Db 1321 GGGAGCTGAATCAATGCAAGAGTGTGATGATGTTTGGAGCTTCAATATGAGATGATG 1380  
QY 1381 AATATTCGTGTTCTTCAAGAAATAGACTTCTGAGGATGATGATGATGATGATG 1440  
Db 1381 AATATTCGTGTTCTTCAAGAAATAGACTTCTGAGGATGATGATGATGATGATG 1440  
QY 1441 TATGTAAGTGAAGAGTCACTCAATCACTGATGAGATGATGATGATGATGATGATG 1500  
Db 1441 TATGTAAGTGAAGAGTCACTCAATCACTGATGAGATGATGATGATGATGATGATG 1500  
QY 1501 TTGGGAAAGCTATGGAAGAGCAAGGCTCCCAACTTAAGCAATGTAAGTGAATATC 1560  
Db 1501 TTGGGAAAGCTATGGAAGAGCAAGGCTCCCAACTTAAGCAATGTAAGTGAATATC 1560  
QY 1561 TAATTAAGAGATTTGTTACTGAGCCACATTAATTAAGAGGCTCCCTACAAATAT 1620  
Db 1561 TAATTAAGAGATTTGTTACTGAGCCACATTAATTAAGAGGCTCCCTACAAATAT 1620  
QY 1621 AATTAAGGTTAAAGAGACATCAATGAGGCTCATCTGAGGATTTATCAAGAAAG 1680  
Db 1621 AATTAAGGTTAAAGAGACATCAATGAGGCTCATCTGAGGATTTATCAAGAAAG 1680

Dh 1620 AATTAAGCGTAAAGAGACCTACATCAGGCGCTTCATCCTGAGATTTTATCAAGAAAG 1679  
Qy 1681 CAGATTTGGCAGTTTCAAAAAGACTCCTGAATATGATTAATCAGGAACTAAACCAAGGAGAC 1740  
Dh 1680 CAGATTTGGCAGTTTCAAAAAGACTCCTGAATATGATTAATCAGGAACTAAACCAAGGAGAC 1739  
Qy 1741 AGAATGCTCAAGTGTGATGATTAATTAATAGTGTGCTGATGAGAAATTAACCAAGGATGAT 1800  
Dh 1740 AGAATGCTCAAGTGTGATGATTAATTAATAGTGTGCTGATGAGAAATTAACCAAGGATGAT 1799  
Qy 1801 CTATTCAGATGAGAAAATCCTAACCCAAATAGAACTACTGCAAAAAGAAATGCTGCTTCA 1860  
Dh 1800 CTATTCAGATGAGAAAATCCTAACCCAAATAGAACTACTGCAAAAAGAAATGCTGCTTCA 1859  
Qy 1861 AAACGAAAGCTGAACCTTAATGAAGCAGAGATATAGCAATATGGAAGTCTGAATTAATATCC 1920  
Dh 1860 AAACGAAAGCTGAACCTTAATGAAGCAGAGATATAGCAATATGGAAGTCTGAATTAATATCC 1919  
Qy 1921 ACAATTTCAAAAGCAGCTTAATAAGAAATAGGCTGAGAGAGAAAGCTTCTACAGGCAATATTC 1980  
Dh 1920 ACAATTTCAAAAGCAGCTTAATAAGAAATAGGCTGAGAGAGAAAGCTTCTACAGGCAATATTC 1979  
Qy 1981 ATGCGCTTGAAGTGTAGTACTAGTAAATCTAAGCCCACTAATTTGTAATGTAATGCAAA 2040  
Dh 1980 ATGCGCTTGAAGTGTAGTACTAGTAAATCTAAGCCCACTAATTTGTAATGTAATGCAAA 2039  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTACAAACCAATGCCAGTCA 2100  
Dh 2040 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGTACAAACCAATGCCAGTCA 2099  
Qy 2101 GGCACAGAGAAACCTTAACATGAGAAAGTAAAGAAACCTGCAACTGAGAGCAAGAAAG 2160  
Dh 2100 GGCACAGAGAAACCTTAACATGAGAAAGTAAAGAAACCTGCAACTGAGAGCAAGAAAG 2159  
Qy 2161 GTAACAGCCCAATGAAGACAGAAATGAAGAAAGCATGACAGCATCTTCCAGAGCTGA 2220  
Dh 2160 GTAACAGCCCAATGAAGACAGAAATGAAGAAAGCATGACAGCATCTTCCAGAGCTGA 2219  
Qy 2221 AGTTAAACAAATGACACTGCTGTTCTTTACTAAGTGTTCAAATACAGTGAATTAAGAAAT 2280  
Dh 2220 AGTTAAACAAATGACACTGCTGTTCTTTACTAAGTGTTCAAATACAGTGAATTAAGAAAT 2279  
Qy 2281 TTGCAATCCAGGCTTCCAGAGAGAAAGAAAGAAAGAAATTAAGAAAGTGAAGT 2340  
Dh 2280 TTGCAATCCAGGCTTCCAGAGAGAAAGAAAGAAAGAAATTAAGAAAGTGAAGT 2339  
Qy 2341 CTAAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAGAACTG 2400  
Dh 2340 CTAAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAGAACTG 2399  
Qy 2401 AAAGATCTGTGAAGATGACAGTATTTCAATGTTGTAAGTGAAGTGAAGTGAAGTGAAGT 2460  
Dh 2400 AAAGATCTGTGAAGATGACAGTATTTCAATGTTGTAAGTGAAGTGAAGTGAAGTGAAGT 2459  
Qy 2461 AAAGATCTGTGTACTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2520  
Dh 2460 AAAGATCTGTGTACTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2519  
Qy 2521 GTGTGAGTCAAGTGTGACAGATTTGAAACCCCAAGGAGCTAATTCATGCTGTTTCCAAAG 2580  
Dh 2520 GTGTGAGTCAAGTGTGACAGATTTGAAACCCCAAGGAGCTAATTCATGCTGTTTCCAAAG 2579  
Qy 2581 ATAAATGAAATGACACAGAGAGGCTTAAAGTATCCATTGGAGATGAAGTGAAGTGAAGT 2640  
Dh 2580 ATAAATGAAATGACACAGAGAGGCTTAAAGTATCCATTGGAGATGAAGTGAAGTGAAGT 2639  
Qy 2641 GGGAAAGAGAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700  
Dh 2640 GGGAAAGAGAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2699  
Qy 2701 TCAAGGTTTCAAGAGGAGCTGATTTGCTGTTTTCAAATCCAGAAATGAGAGAGG 2760  
Dh 2700 TCAAGGTTTCAAGAGGAGCTGATTTGCTGTTTTCAAATCCAGAAATGAGAGAGG 2759

Qy 2761 AATGTGCAACATTCCTGCCCCACTCTGCGCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Dh 2760 AATGTGCAACATTCCTGCCCCACTCTGCGCTTAAAGAAACAAAGTCCAAAGTCACTT 2819  
Qy 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAATGAGTCTTAATATCAAGCTGTAC 2880  
Dh 2820 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAATGAGTCTTAATATCAAGCTGTAC 2879  
Qy 2881 AGACAGTAAATATCACTCAGAGCTTCTGCTGTGCTGAGAAAGATTAAGCCAGTGTATA 2940  
Dh 2880 AGACAGTAAATATCACTCAGAGCTTCTGCTGTGCTGAGAAAGATTAAGCCAGTGTATA 2939  
Qy 2941 ATGCCAAATGTATGATCAAGAGAGCTGAGCTTGTCTATCATCTCAGTTCAGAGGCA 3000  
Dh 2940 ATGCCAAATGTATGATCAAGAGAGCTGAGCTTGTCTATCATCTCAGTTCAGAGGCA 2999  
Qy 3001 ACGAAGCTGAGCTCATCTCTCAATTAAGATGAAGTCTTTCAAACCCATATGCTATAC 3060  
Dh 3000 ACGAAGCTGAGCTCATCTCTCAATTAAGATGAAGTCTTTCAAACCCATATGCTATAC 3059  
Qy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
Dh 3060 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGG 3119  
Qy 3121 AAACCTTGAAGAACATTCATGTCACCTGAAGAGAAATGGCAATGAGAACATTTCCAA 3180  
Dh 3120 AAACCTTGAAGAACATTCATGTCACCTGAAGAGAAATGGCAATGAGAACATTTCCAA 3179  
Qy 3181 GTACAGTGAAGACATTTGCGGTAAATCAATTAAGAAATGTTTAAAGAGCCAGCT 3240  
Dh 3180 GTACAGTGAAGACATTTGCGGTAAATCAATTAAGAAATGTTTAAAGAGCCAGCT 3239  
Qy 3241 CAAGCAATTAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3300  
Dh 3240 CAAGCAATTAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3299  
Qy 3301 TAGGTTCCAGTGAATGAAGAAATTCAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3360  
Dh 3300 TAGGTTCCAGTGAATGAAGAAATTCAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3359  
Qy 3361 ATGCTATGCTAGATTTAGGGGTTTGAACCTGAGGCTAATTAAGAAAGTCTCTGAGAA 3420  
Dh 3360 ATGCTATGCTAGATTTAGGGGTTTGAACCTGAGGCTAATTAAGAAAGTCTCTGAGAA 3419  
Qy 3421 GTAATTTGAACATCTCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3480  
Dh 3420 GTAATTTGAACATCTCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3479  
Qy 3481 ATACAGATTTCTCTCAGATATGATTTCAAGTAACTTAAGAACAGCTTAAGGAAATGATC 3540  
Dh 3480 ATACAGATTTCTCTCAGATATGATTTCAAGTAACTTAAGAACAGCTTAAGGAAATGATC 3539  
Qy 3541 ATGCAATCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGAATTAAGG 3600  
Dh 3540 ATGCAATCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGAATTAAGG 3599  
Qy 3601 AAGATTAATGATTTGCTGAAGAAATGACATTAAGAAAGTCTGCTTTTGAAGAAAGCG 3660  
Dh 3600 AAGATTAATGATTTGCTGAAGAAATGACATTAAGAAAGTCTGCTTTTGAAGAAAGCG 3659  
Qy 3661 TCCAGAAAGAGAGAGCTTGAAGAGAGTCTGAGCTTTCACCCATACATTTGGCTCAGG 3720  
Dh 3660 TCCAGAAAGAGAGAGCTTGAAGAGAGTCTGAGCTTTCACCCATACATTTGGCTCAGG 3719  
Qy 3721 GTTACCGAAGAGGGGCAAGAAATTAAGATTCCTGAGAGAGAACTTCTAGAGAGATG 3780  
Dh 3720 GTTACCGAAGAGGGGCAAGAAATTAAGATTCCTGAGAGAGAACTTCTAGAGAGATG 3779  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTAAGTAAACAAATATACCTTCACT 3840  
Dh 3780 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTAAGTAAACAAATATACCTTCACT 3839







GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: May 27, 1999, 20:03:07 ; Search time 360.2 Seconds

(without alignments)  
2982.836 Million cell updates/sec

Title: US-08-798-691A-3

Perfect score: 5711  
Sequence: 1 AGCTCGCTGAGACTTCCCTGCG.....TCCCCACAGCCACTACTGA 5711

Scoring table: IDENTITY\_NUC

Searched: 240622 seqs, 94065609 residues

Database: N\_Geneseq\_34:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5711	100.0	5914	1	T17493	Mutated BRCA1 codi
2	5711	100.0	5711	1	V64449	Human BRCA1 om12 c
3	5710.6	100.0	5711	1	V64463	Human BRCA1 om12 p
4	5710.6	100.0	5711	1	V64464	Human BRCA1 om12 p
5	5710.6	100.0	5711	1	V64458	Human BRCA1 om12 p
6	5710.6	100.0	5711	1	V64459	Human BRCA1 om12 p
7	5710.6	100.0	5711	1	V64460	Human BRCA1 om12 p
8	5710.6	100.0	5711	1	V64461	Human BRCA1 om12 p
9	5710.6	100.0	5711	1	V64462	Human BRCA1 om12 p
10	5709.4	100.0	5914	1	T18310	BRCA1, breast and
11	5709.4	100.0	5914	1	T17438	BRCA1 coding seque
12	5709.4	100.0	5914	1	T32601	BRCA1, breast and
13	5709.4	100.0	5712	1	T84840	Human breast and o
14	5707.8	99.9	5914	1	T18311	BRCA1 gene nonsens
15	5707.8	99.9	5914	1	T18313	BRCA1 gene missens
16	5707.8	99.9	5914	1	T17445	Mutated BRCA1 codi
17	5707.8	99.9	5914	1	T17446	Mutated BRCA1 codi
18	5707.8	99.9	5914	1	T17449	Mutated BRCA1 codi
19	5707.8	99.9	5914	1	T17453	Mutated BRCA1 codi
20	5707.8	99.9	5914	1	T17457	Mutated BRCA1 codi
21	5707.8	99.9	5914	1	T17462	Mutated BRCA1 codi
22	5707.8	99.9	5914	1	T17466	Mutated BRCA1 codi
23	5707.8	99.9	5914	1	T17468	Mutated BRCA1 codi
24	5707.8	99.9	5914	1	T17471	Mutated BRCA1 codi
25	5707.8	99.9	5914	1	T17476	Mutated BRCA1 codi
26	5707.8	99.9	5914	1	T17478	Mutated BRCA1 codi
27	5707.8	99.9	5914	1	T17479	Mutated BRCA1 codi
28	5707.8	99.9	5914	1	T17481	Mutated BRCA1 codi
29	5707.8	99.9	5914	1	T17483	Mutated BRCA1 codi
30	5707.8	99.9	5914	1	T17484	Mutated BRCA1 codi
31	5707.8	99.9	5914	1	T17486	Mutated BRCA1 codi
32	5707.8	99.9	5914	1	T17489	Mutated BRCA1 codi
33	5707.8	99.9	5914	1	T17490	Mutated BRCA1 codi
34	5707.8	99.9	5914	1	T17491	Mutated BRCA1 codi
35	5707.8	99.9	5914	1	T17492	Mutated BRCA1 codi
36	5707.8	99.9	5914	1	T17494	Mutated BRCA1 codi
37	5707.8	99.9	5914	1	T17495	Mutated BRCA1 codi
38	5707.8	99.9	5914	1	T17496	Mutated BRCA1 codi
39	5707.8	99.9	5914	1	T17497	Mutated BRCA1 codi
40	5707.8	99.9	5914	1	T17498	Mutated BRCA1 codi
41	5707.8	99.9	5914	1	T17499	Mutated BRCA1 codi
42	5707.8	99.9	5914	1	T17500	Mutated BRCA1 codi
43	5707.8	99.9	5914	1	T17501	Mutated BRCA1 codi

44 5707.8 99.9 5914 1 T17502  
45 5707.8 99.9 5711 1 V60569

Mutated BRCA1 codi  
Tumourigenic BRCA1

## ALIGNMENTS

RESULT 1  
T17493 T17493 standard; cDNA; 5914 BP.  
AC T17493:  
DE 02-OCT-1996 (first entry)  
DE Mutated BRCA1 coding sequence from PM06.  
RW Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;  
RW antibody production; germline alteration; probe; lesion neoplasia; human;  
OS gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT cds 120..5711  
FT  
FT /\*tag= a  
FT /product= BRCA1 mutant  
FT 2731  
FT mutation /\*tag= b  
FT /\*note= "C to T mutation"

PN W09605306-A2.  
PD 22-FEB-1996.  
PR 11-AUG-1995; U10202.  
PR 12-AUG-1994; US-289221.  
PR 02-SEP-1994; US-300266.  
PR 16-SEP-1994; US-308104.  
PR 29-NOV-1994; US-348824.  
PR 24-MAR-1995; US-409305.  
PR 07-JUN-1995; US-483553.  
PR 07-JUN-1995; US-480784.  
PA (MYRI-) MYRIAD GENETICS INC.  
PA (CANC-) CANCER INST.  
PA (RECH-) CENT RECH DU CHUL.  
PI Durocher F, Emi M, Nakamura Y, Simard J, Shattuck-Eidens DM;  
DR WPJ; 96-139702/14.  
DR P-PSDB: R81535.  
PT New nucleic acid and polypeptide for mutant or polymorphic BRCA1  
PT gene - for diagnosis and therapy of human breast and ovarian cancer  
PT and for diagnosing pre-disposition to these cancers  
PS Claim 1; 218pp: English.  
CC T17435-T17453 and T17455-T17529 represent mutations of the human breast  
CC and ovarian cancer predisposing gene (BRCA1) (for wild type see T17438).  
CC Proteins encoded by these mutations (see R81483-R81497 and R81499-R81546)  
CC can be used as immunogens for antibody production. These mutant BRCA1  
CC genes have at least 1 mutation or polymorphism in comparison to the wild  
CC type sequence. By detecting a germline alteration in the wild type BRCA1  
CC gene, a predisposition for breast and ovarian cancer can be diagnosed.  
CC In one method, BRCA1 mRNA isolated from a tissue sample from a subject  
CC has a probe, corresponding to a fragment of the wild type sequence (or an  
CC allele-specific probe for one of these mutations), added to it. The  
CC conditions allow for hybridisation of the probe to the mRNA, and any  
CC hybridisation which occurs is detected. Alternatively the BRCA1 gene in  
CC the tissue sample is isolated, and a shift in electrophoretic mobility of  
CC single stranded DNA from the sample on a non-denaturing polyacrylamide  
CC gel indicates a mutation. These methods of detection can also diagnose a  
CC lesion neoplasia associated with the BRCA1 locus. The methods may be  
CC used in gene therapy, protein replacement therapy and protein mimetics,  
CC and may be used to screen for drugs in cancer therapy.  
SQ Sequence 5914 BP; 2006 A; 1155 C; 1316 G; 1437 T;

Query Match 100.0%; Score 5711; DB 1; Length 5914;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCCGAGCCGACGAGCTGTGGGTTCTCAGATTAAGTGAGCC 60  
DB 1 AGCTCGCTGAGACTTCCGAGCCGACGAGCTGTGGGTTCTCAGATTAAGTGAGCC 60

OY	61	CTGGGCTCAGAGGCCCTCACCCCTGCTCTGGGTAAAGTATTGGAACAGAAAGAA	120
Db	61	CTGGGCTCAGAGGCCCTCACCCCTGCTCTGGGTAAAGTATTGGAACAGAAAGAA	120
OY	121	TGGATTATATGCTCTTCGCTTGAAGAGTAAAGTATGATTAATGATATGACGAAA	180
Db	121	TGGATTATATGCTCTTCGCTTGAAGAGTAAAGTATGATTAATGATATGACGAAA	180
OY	181	TCTTAGAGTGTCCCATCTGTCTGAGGTTGATCAAGAACCTGTCTCACAAAGGTGACC	240
Db	181	TCTTAGAGTGTCCCATCTGTCTGAGGTTGATCAAGAACCTGTCTCACAAAGGTGACC	240
OY	241	ACATTTTTTGCAGAAATTTTGCATGCTGAAACTTCTCAACCGAAGAAAGGCCCTCACAGT	300
Db	241	ACATATTTTTGCAGAAATTTTGCATGCTGAAACTTCTCAACCGAAGAAAGGCCCTCACAGT	300
OY	301	GTCCTTATGTAAAGATGATATTAACCAAAAGAGACCCTACAGAAAGTATGAGATTATGTC	360
Db	301	GTCCTTATGTAAAGATGATATTAACCAAAAGAGACCCTACAGAAAGTATGAGATTATGTC	360
OY	361	AACTGTTGAAGAGCTATTTGAAAAATCATTTGTGCTTTACGTTTGACAGAGGTTTGAAGT	420
Db	361	AACTGTTGAAGAGCTATTTGAAAAATCATTTGTGCTTTACGTTTGACAGAGGTTTGAAGT	420
OY	421	ATGCAGAACGCTATATATTTTGCAAAAAAGGAAATTAATCTCCTGAACATCTTAAAGATG	480
Db	421	ATGCAGAACGCTATATATTTTGCAAAAAAGGAAATTAATCTCCTGAACATCTTAAAGATG	480
OY	481	AAGTTTATATCATCCAAAGTATGGGCTACAGAAACCGTGCAGAAACATCTTACAGAGT	540
Db	481	AAGTTTATATCATCCAAAGTATGGGCTACAGAAACCGTGCAGAAACATCTTACAGAGT	540
OY	541	AAACCGAAAAATCCTTCTGTGAGGAAACCAAGTCTCAAGTGTCCAATCTTAAACCTTGGAA	600
Db	541	AAACCGAAAAATCCTTCTGTGAGGAAACCAAGTCTCAAGTGTCCAATCTTAAACCTTGGAA	600
OY	601	CTGTGAGAACCTCTGAGCAACAAGACGGGATACAACTCAAAAGACGTGTCTACATG	660
Db	601	CTGTGAGAACCTCTGAGCAACAAGACGGGATACAACTCAAAAGACGTGTCTACATG	660
OY	661	AATGGGATCTGATTTCTTCTGAAATATACGCTTATTAAGGAACCTTTTTCAGTGTGGAG	720
Db	661	AATGGGATCTGATTTCTTCTGAAATATACGCTTATTAAGGAACCTTTTTCAGTGTGGAG	720
OY	721	ATCAAGAAATTTGTTCAAAATCAACCCCTCAAGAACCAAGGATGAAATCACTTTGGATTCTG	780
Db	721	ATCAAGAAATTTGTTCAAAATCAACCCCTCAAGAACCAAGGATGAAATCACTTTGGATTCTG	780
OY	781	CAAAAAAGGCTGCTTGTGAATTTTCTGACACGATGTAAACAAATACTGATCAATCAAC	840
Db	781	CAAAAAAGGCTGCTTGTGAATTTTCTGACACGATGTAAACAAATACTGATCAATCAAC	840
OY	841	CCAGTAATTAATGATTTGAACCAACCTGAGAGGCTCAGCTGAGAGCATCCAGAAAGT	900
Db	841	CCAGTAATTAATGATTTGAACCAACCTGAGAGGCTCAGCTGAGAGCATCCAGAAAGT	900
OY	901	ATCAGGAGTAGTTCTGTTTCAAACTTGCGATGTGAGCGATGTGGCAACAAATFACTCATGCA	960
Db	901	ATCAGGAGTAGTTCTGTTTCAAACTTGCGATGTGAGCGATGTGGCAACAAATFACTCATGCA	960
OY	961	GCTCATTTACAGCATGAGACAGCATTTATTACTCACTAAAGACAGAAATGATGTAGAA	1020
Db	961	GCTCATTTACAGCATGAGACAGCATTTATTACTCACTAAAGACAGAAATGATGTAGAA	1020
OY	1021	AGGCTGAATTTCTGTATATTAAGCAACAGCCTTGCTTAGCAAGAGCCAACTTAACAGAT	1080
Db	1021	AGGCTGAATTTCTGTATATTAAGCAACAGCCTTGCTTAGCAAGAGCCAACTTAACAGAT	1080
OY	1081	GGGCTGGAAGTAAAGAAACATGTAAAGATAGGGGAGCTCCAGACAGAAAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAAGAAACATGTAAAGATAGGGGAGCTCCAGACAGAAAAAAAGGTAG	1140
OY	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAATAGCAAGAAATGCTCATCT	1200

Db	1141	ATCTAAATGCTGATCCCTCTGTGTAGGAAAGAAATGAAATAGCAAGAACTGCCACTCT	1200
Qy	1201	CAGAGAAATCCTAGAGATACCTGAGATGTTCTCTTGATTAACACTAATAATAGCAGACTTCAGA	1260
Db	1201	CAGAGAAATCCTAGAGATACCTGAGATGTTCTCTTGATTAACACTAATAATAGCAGACTTCAGA	1260
Qy	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTATGTAAGTGTAGGTTCTGATGTCATCATATGATG	1320
Db	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTATGTAAGTGTAGGTTCTGATGTCATCATATGATG	1320
Qy	1321	GGGAGCTCGAATCAAAATGCCAAAGTACTGATATATGGACGTTCTCAATGAGTGAATG	1380
Db	1321	GGGAGCTCGAATCAAAATGCCAAAGTACTGATATATGGACGTTCTCAATGAGTGAATG	1380
Qy	1381	AATATTCGTGTTCTTCAGAGAAATAACATTAAGTGGCCAGTGTATCCTCATGAGGCTTTAA	1440
Db	1381	AATATTCGTGTTCTTCAGAGAAATAACATTAAGTGGCCAGTGTATCCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGATTAATATGAGACAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGATTAATATGAGACAAATAT	1500
Qy	1501	TTGGGAAAACTATCCGGAAGAAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAATAATC	1560
Db	1501	TTGGGAAAACTATCCGGAAGAAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAATAATC	1560
Qy	1561	TAAATATAGAGACATTTGTTACTGAGCAAGATTAATCAAGAGCGTCCCTCCCAATA	1620
Db	1561	TAAATATAGAGACATTTGTTACTGAGCAAGATTAATCAAGAGCGTCCCTCCCAATA	1620
Qy	1621	AATTAAGCGTAAAGAGAGACACTACATCAGGCGTTCATCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AATTAAGCGTAAAGAGAGACACTACATCAGGCGTTCATCTGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCTCGAAATGATTAATAGGGAACCTAACCAAGGAGGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAGACTCTCGAAATGATTAATAGGGAACCTAACCAAGGAGGC	1740
Qy	1741	AGAAATGCTCAAGTATGATATATTAATGATGATGATGATGATGATGATGATGATGATGATG	1800
Db	1741	AGAAATGCTCAAGTATGATATATTAATGATGATGATGATGATGATGATGATGATGATGATG	1800
Qy	1801	CTATTCAGAAATGAGAAAAATCCTAACCCATAGAAATCACTCCAAAAAGAAATCTGCTTCA	1860
Db	1801	CTATTCAGAAATGAGAAAAATCCTAACCCATAGAAATCACTCCAAAAAGAAATCTGCTTCA	1860
Qy	1861	AAAGGAAAGCTGAACCTATTAAGCAGCATTAAGCAATATGGAATCTCGAATTTAATATCC	1920
Db	1861	AAAGGAAAGCTGAACCTATTAAGCAGCATTAAGCAATATGGAATCTCGAATTTAATATCC	1920
Qy	1921	ACAATTCAAAAGGCAACCTTAAGAAATTAAGGCTGAGGAGAGCTTCATACCGGCAATATTC	1980
Db	1921	ACAATTCAAAAGGCAACCTTAAGAAATTAAGGCTGAGGAGAGCTTCATACCGGCAATATTC	1980
Qy	1981	ATGCGCTGAACTAGTAGTCAAGTAAATCTAAAGCCACCTATTTGTAAGTAAATGCAAA	2040
Db	1981	ATGCGCTGAACTAGTAGTCAAGTAAATCTAAAGCCACCTATTTGTAAGTAAATGCAAA	2040
Qy	2041	TTGATAGTTGTTCTTACGAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGCGCACTCA	2100
Db	2041	TTGATAGTTGTTCTTACGAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGCGCACTCA	2100
Qy	2101	GGCAGACAGAAACCTTAACAATCTATGGAAGGTTAAAGAACCTGCAACTGGAACCAAGAGA	2160
Db	2101	GGCAGACAGAAACCTTAACAATCTATGGAAGGTTAAAGAACCTGCAACTGGAACCAAGAGA	2160
Qy	2161	GTAACAAGCCAAATGAACACAAAGTAAAGACATGACAGGATCTCTTCCACAGAGCGGA	2220
Db	2161	GTAACAAGCCAAATGAACACAAAGTAAAGACATGACAGGATCTCTTCCACAGAGCGGA	2220
Qy	2221	AGTTAACAAATGCACCTGTTCTTTTACTAAGTGTGTCAAAATCCAGTACACTTAAAGAT	2280

```
Db 2221 AGTTAAACAAATGCACCTGGTTCCTTTACTAAGTGTCAAAATACCAATGCAATTAAGAAAT 2280
QY 2281 TTGTCAATCCTAGCCTTCCAGAGAGAGAAAAAGAGAAAACTAGAAAACAGTTAAAGTGT 2340
Db 2281 TTGTCAATCCTAGCCTTCCAGAGAGAGAAAAAGAGAAAACTAGAAAACAGTTAAAGTGT 2340
QY 2341 CTATATATGCTGAAGACCCCAAAAGATCTCATGTTAACTGGAGAAAGGTTTGTGAAACTG 2400
Db 2341 CTATATATGCTGAAGACCCCAAAAGATCTCATGTTAACTGGAGAAAGGTTTGTGAAACTG 2400
QY 2401 AAAGATCTGTAGAGAGTAGAGATTTTCATTTGTGACTGTGACTGATTATAGCACTAGG 2460
Db 2401 AAAGATCTGTAGAGAGTAGAGATTTTCATTTGTGACTGTGACTGATTATAGCACTAGG 2460
QY 2461 AAAGTATCTGCTTACTGGAAGTTAGACACTGTAGGGAAGCAAAAAACAGAACCAATTAAT 2520
Db 2461 AAAGTATCTGCTTACTGGAAGTTAGACACTGTAGGGAAGCAAAAAACAGAACCAATTAAT 2520
QY 2521 GTGTGACTGCTGTGAGCATTTGAAAAACCCCAAGGACTTAATTCATGTTGTCCAAAG 2580
Db 2521 GTGTGACTGCTGTGAGCATTTGAAAAACCCCAAGGACTTAATTCATGTTGTCCAAAG 2580
QY 2581 ATATATAGAAATGACACAGAGAGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC 2640
Db 2581 ATATATAGAAATGACACAGAGAGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC 2640
QY 2641 GGGAAACAAACATAGAAATGGAAGAAAGTGAATCTGATGCTCACTATTTCAGAAATCAT 2700
Db 2641 GGGAAACAAACATAGAAATGGAAGAAAGTGAATCTGATGCTCACTATTTCAGAAATCAT 2700
QY 2701 TCAAGGTTTAAAGGCGGCATCTTGTCTGTTTCAAAATCCAGAAATGACAGAGAGG 2760
Db 2701 TCAAGGTTTAAAGGCGGCATCTTGTCTGTTTCAAAATCCAGAAATGACAGAGAGG 2760
QY 2761 AATGTGCAACATTTCTGCGCCACTCTGCGTCTTAAGAAACAAAGCCAAAGATCACTT 2820
Db 2761 AATGTGCAACATTTCTGCGCCACTCTGCGTCTTAAGAAACAAAGCCAAAGATCACTT 2820
QY 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTAC 2880
Db 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTAC 2880
QY 2881 AGACAGTAAATATACACGACGAGGCTTCTGCTGTTGCTCAGAAAGATTAAGCCAGTTATA 2940
Db 2881 AGACAGTAAATATACACGACGAGGCTTCTGCTGTTGCTCAGAAAGATTAAGCCAGTTATA 2940
QY 2941 ATGCCAAATGTAGATCAAAAGAGAGCTCTAGGTTTGTGCTATCATCTCAGTTCAGAGCA 3000
Db 2941 ATGCCAAATGTAGATCAAAAGAGAGCTCTAGGTTTGTGCTATCATCTCAGTTCAGAGCA 3000
QY 3001 ACGAAATCTGACTCTATTACTCCAAATTAACATGAGACTTTTACAAACCCATATGCTATAC 3060
Db 3001 ACGAAATCTGACTCTATTACTCCAAATTAACATGAGACTTTTACAAACCCATATGCTATAC 3060
QY 3061 CACCACCTTTTCCCATCAATGACTATTTTAAACTAAATGTAGAAAAATCTGCTAGAGG 3120
Db 3061 CACCACCTTTTCCCATCAATGACTATTTTAAACTAAATGTAGAAAAATCTGCTAGAGG 3120
QY 3121 AAAACTTTGAGGAACATTCATGTCACCTGAAGAGAAATGGGAAATGAGAACTTCGAA 3180
Db 3121 AAAACTTTGAGGAACATTCATGTCACCTGAAGAGAAATGGGAAATGAGAACTTCGAA 3180
QY 3181 GTACAGTAGACACAAATTAAGCCGTAATTAACATTAAGAAAAATGTTTTTAAAGAACCCAGCT 3240
Db 3181 GTACAGTAGACACAAATTAAGCCGTAATTAACATTAAGAAAAATGTTTTTAAAGAACCCAGCT 3240
QY 3241 CAAGCATATTAATGAAGTAGTTCGCTACTAATGAAGTGGGCTCCAGTAATTAAGTAA 3300
Db 3241 CAAGCATATTAATGAAGTAGTTCGCTACTAATGAAGTGGGCTCCAGTAATTAAGTAA 3300
QY 3301 TAGGTTCCAGTAGATGAAGAAATTCAGACAGAACTAGGTAGAAACAGAGGGCCAAATTTGA 3360
Db 3301 TAGGTTCCAGTAGATGAAGAAATTCAGACAGAACTAGGTAGAAACAGAGGGCCAAATTTGA 3360
QY 3361 ATGCTATGCTTAAGATTAGAGGGTTTGGCAACCTGAGGCTATTAACAAAGTCTTCGGAA 3420
Db 3361 ATGCTATGCTTAAGATTAGAGGGTTTGGCAACCTGAGGCTATTAACAAAGTCTTCGGAA 3420
QY 3421 GTAAATGTATAGCATTCCTGGAATTAAGAAAGAAATTAAGAAAGTGTACAGACTGTA 3480
Db 3421 GTAAATGTATAGCATTCCTGGAATTAAGAAAGAAATTAAGAAAGTGTGTACAGACTGTA 3480
QY 3481 ATACAGATTTCTCTCCATATCTGATTGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAG 3540
Db 3481 ATACAGATTTCTCTCCATATCTGATTGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAG 3540
QY 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTGAATTAAGG 3600
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTGAATTAAGG 3600
QY 3601 AAGATATCTATTTTGTGGAATAAGCATTAAGAAAGTTCGCTGTTTTAGCAAAAGCG 3660
Db 3601 AAGATATCTATTTTGTGGAATAAGCATTAAGAAAGTTCGCTGTTTTAGCAAAAGCG 3660
QY 3661 TCCAGAAAGAGAGCTTAGCAGAGAGTCCAGCCCTTACCCATACATTTGGCTCAGG 3720
Db 3661 TCCAGAAAGAGAGCTTAGCAGAGAGTCCAGCCCTTACCCATACATTTGGCTCAGG 3720
QY 3721 GTTAACGGAAGAGGGGCCAAGAAATTAAGAGTCTCAGAAAGAACTTATCTAGTAGAGATG 3780
Db 3721 GTTAACGGAAGAGGGGCCAAGAAATTAAGAGTCTCAGAAAGAACTTATCTAGTAGAGATG 3780
QY 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGGTAAAGTAAACATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGGTAAAGTAAACATATACCTTCTCAGT 3840
QY 3841 CTACTAGGCAATACACGCTGTGCTACGAGAGTCTGCTTAAGAAACACAGAGAGAAATTA 3900
Db 3841 CTACTAGGCAATACACGCTGTGCTACGAGAGTCTGCTTAAGAAACACAGAGAGAAATTA 3900
QY 3901 TATCATTTGAAGAAATAGCTTAATTAAGTCACTGAGTAACAGGTAATTTGGCAAGGCACTTC 3960
Db 3901 TATCATTTGAAGAAATAGCTTAATTAAGTCACTGAGTAACAGGTAATTTGGCAAGGCACTTC 3960
QY 3961 AGGAACATCACCTTATGTAGAGAAACAAATGTTCTGCTACCTGTTTCTTACAGTGCA 4020
Db 3961 AGGAACATCACCTTATGTAGAGAAACAAATGTTCTGCTACCTGTTTCTTACAGTGCA 4020
QY 4021 GTGAATTTGGAAGACTGACAGCAATTAACAAACCCAGATCCCTTCTTATGTTGTTCTT 4080
Db 4021 GTGAATTTGGAAGACTGACAGCAATTAACAAACCCAGATCCCTTCTTATGTTGTTCTT 4080
QY 4081 CCAAAACAAATGAGGCACTCACTGAAAAGCCAGGAGTTGGTCTGAGTACAGAAATTTGG 4140
Db 4081 CCAAAACAAATGAGGCACTCACTGAAAAGCCAGGAGTTGGTCTGAGTACAGAAATTTGG 4140
QY 4141 TTTCAGATGATGAAGAAAGAGAAAGGAGGCTTGGAGAAATTAATCAAGAAAGACCAAGCA 4200
Db 4141 TTTCAGATGATGAAGAAAGAGAAAGGAGGCTTGGAGAAATTAATCAAGAAAGACCAAGCA 4200
QY 4201 TGGATTTCAAACCTTAGGGAAGAGAGCACTGCGGTGAGTGAAGAAACAAAGGCTCTGAAG 4260
Db 4201 TGGATTTCAAACCTTAGGGAAGAGAGCACTGCGGTGAGTGAAGAAACAAAGGCTCTGAAG 4260
QY 4261 ACTGCTCAGGCTATCTCTCAGAGTAGACATTTTAAACCACTCAGCAGAGAGATACCATG 4320
Db 4261 ACTGCTCAGGCTATCTCTCAGAGTAGACATTTTAAACCACTCAGCAGAGAGATACCATG 4320
QY 4321 AACATTAACCTGATTAAGAGCTCCAGCAGAGAAATGGCTGAACTAGAACTGTGTGAACAGC 4380
Db 4321 AACATTAACCTGATTAAGAGCTCCAGCAGAGAAATGGCTGAACTAGAACTGTGTGAACAGC 4380
QY 4381 ATGGAGGCGAGCCTTCTTAACAGTACCTTCATCAATGAAGTGACTCTTTCGCCCTTGAGG 4440
Db 4381 ATGGAGGCGAGCCTTCTTAACAGTACCTTCATCAATGAAGTGACTCTTTCGCCCTTGAGG 4440
```

```

QY 4441 ACCTGCAAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTAACTTACAGAAAAAGTA 4500
    |||
Db 4441 ACCGCAAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTAACTTACAGAAAAAGTA 4500
QY 4501 GTGAAATACCCATTAAGCAGAAATCCAGAAAGGCTTCTGCTGACAAAGTTTGAGGTCTG 4560
    |||
Db 4501 GTGAAATACCCATTAAGCAGAAATCCAGAAAGGCTTCTGCTGACAAAGTTTGAGGTCTG 4560
QY 4561 CAGATAGTCTTACAGAGTAAAAATTAAGAACAGAGAGTGAAGAGTCAATCCCTTCTAAAT 4620
    |||
Db 4561 CAGATAGTCTTACAGAGTAAAAATTAAGAACAGAGAGTGAAGAGTCAATCCCTTCTAAAT 4620
QY 4621 GCCCATCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680
    |||
Db 4621 GCCCATCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680
QY 4681 ACTACCATCATCAAGAGAGAGTCAATTAAGTGTGATGATGATGATGATGATGATGATGATGAT 4740
    |||
Db 4681 ACTACCATCATCAAGAGAGAGTCAATTAAGTGTGATGATGATGATGATGATGATGATGATGAT 4740
QY 4741 AGTCTGGGCGCACAGATTTGACAGGAAACATCTTACTTGCACAGGCAAGATCTAGAGGAA 4800
    |||
Db 4741 AGTCTGGGCGCACAGATTTGACAGGAAACATCTTACTTGCACAGGCAAGATCTAGAGGAA 4800
QY 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTTCTCTGATGATGATGATGATGATGATGATGATGAT 4860
    |||
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTTCTCTGATGATGATGATGATGATGATGATGATGAT 4860
QY 4861 AAGACAGAGCCCGACAGATCAGCTGCTGTGGCAACATACATCTTCAACCTCTGATGATGATGAT 4920
    |||
Db 4861 AAGACAGAGCCCGACAGATCAGCTGCTGTGGCAACATACATCTTCAACCTCTGATGATGATGAT 4920
QY 4921 AAGTCCCAATTTGAAAGTTGACAGATCTGCGCCAGATGCGTCTGATGATGATGATGATGATGAT 4980
    |||
Db 4921 AAGTCCCAATTTGAAAGTTGACAGATCTGCGCCAGATGCGTCTGATGATGATGATGATGATGAT 4980
QY 4981 ATCTGTGGTGTAAATGACATGGAAGTGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040
    |||
Db 4981 ATCTGTGGTGTAAATGACATGGAAGTGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040
QY 5041 CTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5100
    |||
Db 5041 CTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5100
QY 5101 AATTTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5160
    |||
Db 5101 AATTTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5160
QY 5161 CTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5220
    |||
Db 5161 CTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5220
QY 5221 TGAATATTTTCTAGGAATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5280
    |||
Db 5221 TGAATATTTTCTAGGAATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5280
QY 5281 AGCTATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5340
    |||
Db 5281 AGCTATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5340
QY 5341 TCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5400
    |||
Db 5341 TCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5400
QY 5401 TCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5460
    |||
Db 5401 TCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5460
QY 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5520
    |||
Db 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5520
QY 5521 GCACAGGTGTCCACCAATTTGTGTGTGACAGCAGATGCTGACAGAGAGAGAGAGAGAGAGAG 5580
    |||

```

```

Db 5521 GCACAGGTGTCCACCAATTTGTGTGTGACAGCAGATGCTGACAGAGAGAGAGAGAGAGAG 5580
QY 5581 TCATGCAATTTGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5640
    |||
Db 5581 TCATGCAATTTGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5640
QY 5641 GTGAGACACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
    |||
Db 5641 GTGAGACACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
QY 5701 GCCCACTACTGA 5711
    |||
Db 5701 GCCCACTACTGA 5711
    |||

RESULT 2
V46449
ID V46449 standard; cDNA: 5711 BP.
AC V46449;
DT 18-NOV-1998 (first entry)
DE Human BRCA1 om12 cDNA.
KW BRCA1; om12: human; breast and ovarian cancer predisposing gene;
    polymorphism; susceptibility; anti-oncogene; tumour suppressor;
    chromosome 17q; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 120..5711
    /tag= a
    /product= "BRCA1 om12 protein"
PN US5750400-A.
PD 12-MAY-1998.
PF 12-FEB-1997: 798691.
PR 12-FEB-1996: US-598591.
PS 12-FEB-1997: US-798691.
PA (ONCO-) ONCORMED INC.
PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,
    Schelter DB, Zeng B;
    WPI: 98-296774/26.
DR P-PSDB: W76099.
PT BRCA1 om1 gene coding sequences - useful for distinguishing between
    PT polymorphisms and mutation(s) in the screening for disposition to
    breast or ovarian cancer
PS Claim 2d: Column 41-46: 54pp; English.
CC This sequence encodes the human BRCA1 (breast and ovarian cancer
    predisposing gene) om12 gene. This sequence and polymorphic variations of
    CC this sequence are useful for the identification of an individual who may
    CC or may not have an increased susceptibility to breast or ovarian cancer.
    CC The sequences used identify gene changes which are due to polymorphisms,
    CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
    CC suppressor) which is involved in genetic inheritance of cancers,
    CC especially breast and ovarian cancer. It is found at human chromosome 17q
    CC which is known to be linked to cancer susceptibility, especially breast
    CC cancer. Cells containing a mutation in this gene lose the wild-type
    CC function of BRCA1 and are more susceptible to cancers.
SQ Sequence 5711 bp: 1956 A; 1098 C; 1274 G; 1383 T;

Query Match 100.0%; Score 5711; DB 1; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGCTGAGACTTCTGAGACCCCGACAGAGCTGTGGGTTTCTCAGATACTGGGCC 60
    |||
Db 1 AGCTGCTGAGACTTCTGAGACCCCGACAGAGCTGTGGGTTTCTCAGATACTGGGCC 60
QY 61 CCTGCGCTCAGAGAGGCTTACCTCTGCTGTGGTAAAGTTCATTGGAACAGAAAGAA 120
    |||
Db 61 CCTGCGCTCAGAGAGGCTTACCTCTGCTGTGGTAAAGTTCATTGGAACAGAAAGAA 120
QY 121 TGGATTATCTGCTCTTCCGCTGGAAGAGTACAAATATCTATATGATGCGAAAA 180
    |||
Db 121 TGGATTATCTGCTCTTCCGCTGGAAGAGTACAAATATCTATATGATGCGAAAA 180

```

181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAGAGACCTGTCTCCACAAAGTGTGACC 240  
182 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAGAGACCTGTCTCCACAAAGTGTGACC 240  
183 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAGAGACCTGTCTCCACAAAGTGTGACC 240  
241 ACATATTTTGCAAATTTTGATGATGCTGAACTTCTCAACGAGAAAGGAGGCTTGCAGT 300  
242 ACATATTTTGCAAATTTTGATGATGCTGAACTTCTCAACGAGAAAGGAGGCTTGCAGT 300  
243 ACATATTTTGCAAATTTTGATGATGCTGAACTTCTCAACGAGAAAGGAGGCTTGCAGT 300  
301 GTCCCTTATGTAAGATGATATTAACCAAGAGAGCTTACAGAGAAAGTATGAGATTTAGTC 360  
302 GTCCCTTATGTAAGATGATATTAACCAAGAGAGCTTACAGAGAAAGTATGAGATTTAGTC 360  
303 GTCCCTTATGTAAGATGATATTAACCAAGAGAGCTTACAGAGAAAGTATGAGATTTAGTC 360  
361 AACTTGTGAAGAGCTATTTGAAAAATCATTTGTGCTTTTCACTTGAACAGAGTTTGAGT 420  
362 AACTTGTGAAGAGCTATTTGAAAAATCATTTGTGCTTTTCACTTGAACAGAGTTTGAGT 420  
421 ATGCCAAACAGCTATATTTTGCAAAAAAGAAATTAACCTCTCTGAACATCTTAAAGATG 480  
422 ATGCCAAACAGCTATATTTTGCAAAAAAGAAATTAACCTCTCTGAACATCTTAAAGATG 480  
481 AAGTTTCTATCATCCAAAGATGGCTACAGAAACCGTGCAGAAAGATCTTACAGAGT 540  
482 AAGTTTCTATCATCCAAAGATGGCTACAGAAACCGTGCAGAAAGATCTTACAGAGT 540  
483 AAGTTTCTATCATCCAAAGATGGCTACAGAAACCGTGCAGAAAGATCTTACAGAGT 540  
541 AACCCGAAAAATCCTTCTCTGACAGAAACCAAGTCTCAGTGTCCAATCTCTAACCTTGGAA 600  
542 AACCCGAAAAATCCTTCTCTGACAGAAACCAAGTCTCAGTGTCCAATCTCTAACCTTGGAA 600  
601 CTTGTGAAGCTGTGAGCAAAAGCAGCGATNCAACCTCAAAAGAGCTGTCTTACATG 660  
602 CTTGTGAAGCTGTGAGCAAAAGCAGCGATNCAACCTCAAAAGAGCTGTCTTACATG 660  
661 AATTGGATCTGATTTCTTGAAGATACCGTTATTAAGCAATCTTATTCAGTGTGGAG 720  
662 AATTGGATCTGATTTCTTGAAGATACCGTTATTAAGCAATCTTATTCAGTGTGGAG 720  
721 ATCAGAGATTTGTTACAATAACCCCTCAAGAGAACAGAGGATGAATCACTGTTGGATTCTG 780  
722 ATCAGAGATTTGTTACAATAACCCCTCAAGAGAACAGAGGATGAATCACTGTTGGATTCTG 780  
781 CAAAAAGGCTGTGTGAAATTTCTGAGACGAGATGTAAACAAATATCTGAACATCATCAAC 840  
782 CAAAAAGGCTGTGTGAAATTTCTGAGACGAGATGTAAACAAATATCTGAACATCATCAAC 840  
841 CCAGTAAATATGATTTGGAACACCACTGAGAGAGCTGACGTGAGAGCATCCAGAAAAGT 900  
842 CCAGTAAATATGATTTGGAACACCACTGAGAGAGCTGACGTGAGAGCATCCAGAAAAGT 900  
901 ATCAGGATGATCTGTCTTCAAACTTCATGTGAGAGCATGTGGCAGCAAAATCTCATGCA 960  
902 ATCAGGATGATCTGTCTTCAAACTTCATGTGAGAGCATGTGGCAGCAAAATCTCATGCA 960  
961 GGTCAATTAAGCATGAGACAGAGATTTATCTACTATAAGCAGAAATGAATGTGAAA 1020  
962 GGTCAATTAAGCATGAGACAGAGATTTATCTACTATAAGCAGAAATGAATGTGAAA 1020  
1021 AGGCTGAATTTCTGTATTAAGCAACAGCTGTGCTTAGAGAGAGCCAAATATGAGAT 1080  
1022 AGGCTGAATTTCTGTATTAAGCAACAGCTGTGCTTAGAGAGAGCCAAATATGAGAT 1080  
1081 GGGCTGGAAGTAAGAGAAACATGTATGATAGGGGAGCTCCACAGACAGAAAAAGGTAG 1140  
1082 GGGCTGGAAGTAAGAGAAACATGTATGATAGGGGAGCTCCACAGACAGAAAAAGGTAG 1140  
1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATTAAGCAAAAGTCCATGCT 1200  
1142 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATTAAGCAAAAGTCCATGCT 1200  
1201 CAGAGAAATCTAGAGATCTAGAGAGATGTTCTTGGATTAACACTTAATATGAGCATTCAGA 1260  
1202 CAGAGAAATCTAGAGATCTAGAGAGATGTTCTTGGATTAACACTTAATATGAGCATTCAGA 1260

1261 AAGTAAATGAGTGTCTTTCAGAAAGATGAACTGTAGGTTCTGATGATCTCAATGATG 1320  
1262 AAGTAAATGAGTGTCTTTCAGAAAGATGAACTGTAGGTTCTGATGATCTCAATGATG 1320  
1321 GGGAGCTGAATCAAAATGCGAAAGTATGATGTATTTGAGCTTCTCAATGAGATGATG 1380  
1322 GGGAGCTGAATCAAAATGCGAAAGTATGATGTATTTGAGCTTCTCAATGAGATGATG 1380  
1323 GGGAGCTGAATCAAAATGCGAAAGTATGATGTATTTGAGCTTCTCAATGAGATGATG 1380  
1381 AATATTCTGTTCTTTCAGAAAGATGAACTGTAGGCTGAGATCTCATGAGGCTTTAA 1440  
1382 AATATTCTGTTCTTTCAGAAAGATGAACTGTAGGCTGAGATCTCATGAGGCTTTAA 1440  
1441 TATGTAAAGTGAAGAGTTCCTCAATTCAGTAGAGATTAATTTGAAGCAAAATAT 1500  
1442 TATGTAAAGTGAAGAGTTCCTCAATTCAGTAGAGATTAATTTGAAGCAAAATAT 1500  
1501 TTGGGAAAACCTATGGAAGAGGCAAGGCTCCCAACTTAAGCCATGATAGCAAAATC 1560  
1502 TTGGGAAAACCTATGGAAGAGGCAAGGCTCCCAACTTAAGCCATGATAGCAAAATC 1560  
1503 TTGGGAAAACCTATGGAAGAGGCAAGGCTCCCAACTTAAGCCATGATAGCAAAATC 1560  
1561 TAATTTAGAGCAATTTGTTACTGAGCCACAGATATATACAGAGCGTCCCTCACAAATA 1620  
1562 TAATTTAGAGCAATTTGTTACTGAGCCACAGATATATACAGAGCGTCCCTCACAAATA 1620  
1621 AATTTAAGCGTAAAGAGAGACCTACATCAGGCTTCATCTGAGATTTTATCAGAAAG 1680  
1622 AATTTAAGCGTAAAGAGAGACCTACATCAGGCTTCATCTGAGATTTTATCAGAAAG 1680  
1681 CAGATTTGGAGTTCAAAAGATCCCGAAATGATTAATCAGGGAATTAACCAAGGAGAC 1740  
1682 CAGATTTGGAGTTCAAAAGATCCCGAAATGATTAATCAGGGAATTAACCAAGGAGAC 1740  
1741 AGAATGGTCAAGTGAATGAATATTAATAGTGTGATGATGATTAACCAAGGAGAT 1800  
1742 AGAATGGTCAAGTGAATGAATATTAATAGTGTGATGATGATTAACCAAGGAGAT 1800  
1801 CTATTCAAGATGAGAAATTCCTAACCAATAGATCACTCGAAAAAGATCTGCTTTA 1860  
1802 CTATTCAAGATGAGAAATTCCTAACCAATAGATCACTCGAAAAAGATCTGCTTTA 1860  
1861 AAACGAAAGCTGAACTATTAACAGAGATTAAGCAATTTGGAACCTGAAATTAATATC 1920  
1862 AAACGAAAGCTGAACTATTAACAGAGATTAAGCAATTTGGAACCTGAAATTAATATC 1920  
1921 ACAATTCAAAAGCAGCTTAAAGAAATAGGCTGAGAGAGTCTTCTTACAGGATATTC 1980  
1922 ACAATTCAAAAGCAGCTTAAAGAAATAGGCTGAGAGAGTCTTCTTACAGGATATTC 1980  
1981 ATGCGTTGAAGTATGATGATGAGAAATCTAAGCCACCTAATGTACTGAATTCAAA 2040  
1982 ATGCGTTGAAGTATGATGATGAGAAATCTAAGCCACCTAATGTACTGAATTCAAA 2040  
2041 TTGATATGTTGTTCTGCAAGATGAAGATTAAGAAAAAGTAAAGCAAAAGTCCAGTCA 2100  
2042 TTGATATGTTGTTCTGCAAGATGAAGATTAAGAAAAAGTAAAGCAAAAGTCCAGTCA 2100  
2101 GGCACAGCAGAAACCTACATCATGAGAGTAAAGAACTCTCAACTGAGAGCAAGAGA 2160  
2102 GGCACAGCAGAAACCTACATCATGAGAGTAAAGAACTCTCAACTGAGAGCAAGAGA 2160  
2161 GTTACAGCAGAAATGAGACAGCAAGTAAAGACATGACAGCATCTTCCAGAGAGCTGA 2220  
2162 GTTACAGCAGAAATGAGACAGCAAGTAAAGACATGACAGCATCTTCCAGAGAGCTGA 2220  
2221 AGTTAAACAATGACACTGTTCTTTTACTAAGATGTTCAAAATCCAGTGAACCTTAAAGAT 2280  
2222 AGTTAAACAATGACACTGTTCTTTTACTAAGATGTTCAAAATCCAGTGAACCTTAAAGAT 2280  
2281 TTGTCAATCTAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 2340  
2282 TTGTCAATCTAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 2340  
2341 CTAATTAATGCTGAAGAGACCCCAAGATCTCATGTTAAGTGGAGAGAGAGGTTTTCAGAACTG 2400

|||||  
Db 2341 CTAATAATGCTAAGACCCCAAGATCATGTTAAGTGGAGAAAGGTTTCCAAACTG 2400  
QY 2401 AAGATCTGTAGAGATGACAGTATTTTCATTTGGTACCTGGTACTGATTAAGCACTCAGG 2460  
Db 2401 AAGATCTGTAGAGATGACAGTATTTTCATTTGGTACCTGGTACTGATTAAGCACTCAGG 2460  
QY 2461 AAGATCTCTGTTACTGGAAGTTAGCATCTTAGGGAAGGCAAAAACAGAACCAATTAAT 2520  
Db 2461 AAGATCTCTGTTACTGGAAGTTAGCATCTTAGGGAAGGCAAAAACAGAACCAATTAAT 2520  
QY 2521 GTGTAGTCAGTGTGAGCATTTGAAACCCCAAGGACTAATTCATGGTGTGTTCCAAAG 2580  
Db 2521 GTGTAGTCAGTGTGAGCATTTGAAACCCCAAGGACTAATTCATGGTGTGTTCCAAAG 2580  
QY 2581 ATAAATAGAAATGACACAGAAAGCTTTAAGTATCCATTTGGACATGAAGTTAACACAGTC 2640  
Db 2581 ATAAATAGAAATGACACAGAAAGCTTTAAGTATCCATTTGGACATGAAGTTAACACAGTC 2640  
QY 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTAACTTATGCTCATATTTCAGAAATACAT 2700  
Db 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTAACTTATGCTCATATTTCAGAAATACAT 2700  
QY 2701 TCAAGGTTTCAAAAGGCGCCAGTATTTGCTGTTTCAATCCAGGAAATGCAAGAGG 2760  
Db 2701 TCAAGGTTTCAAAAGGCGCCAGTATTTGCTGTTTCAATCCAGGAAATGCAAGAGG 2760  
QY 2761 AATGTGCAACATCTCTGCGCCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATCTCTGCGCCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAAGAGAAATCAAGGAAAGATAGTATATTCAGACCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAAGAGAAATCAAGGAAAGATAGTATATTCAGACCTGTAC 2880  
QY 2881 AGACAGTTAATATCACTGAGGCTTCTCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGAGGCTTCTCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA 2940  
QY 2941 ATGCCAAATGTAGTATCAAAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000  
QY 3001 AGCAAACTGGAGTCAATCTCAAAATTAACATGAACTTTTACAAACCCATATCCGATAC 3060  
Db 3001 AGCAAACTGGAGTCAATCTCAAAATTAACATGAACTTTTACAAACCCATATCCGATAC 3060  
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTTAATGTAAGAAATCTGCTAGAGG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTTAATGTAAGAAATCTGCTAGAGG 3120  
QY 3121 AAAACTTTGAGGACATTCATATGTCACCTGAAAGAGAAATGGGAAATGGAACATTTCAA 3180  
Db 3121 AAAACTTTGAGGACATTCATATGTCACCTGAAAGAGAAATGGGAAATGGAACATTTCAA 3180  
QY 3181 GTACAGTAGAGCAATTTAGCCGCTAATTAACATTAAGAAAAATGTTTTAAAGAACCCAGCT 3240  
Db 3181 GTACAGTAGAGCAATTTAGCCGCTAATTAACATTAAGAAAAATGTTTTAAAGAACCCAGCT 3240  
QY 3241 CAAGCAATATTAAAGAGTGTCCAGTCAATTAATGAATGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATATTAAAGAGTGTCCAGTCAATTAATGAATGGGCTCCAGTATTAATGAAA 3300  
QY 3301 TAGGTTCCAGTGAATGAAGTGTTCAGAGTAAAGAAATGGGCTCCAGTATTAATGAAA 3360  
Db 3301 TAGGTTCCAGTGAATGAAGTGTTCAGAGTAAAGAAATGGGCTCCAGTATTAATGAAA 3360  
QY 3361 ATGCTATGCTTAGATTAGGGGTTTGGCAACCTGAGTCTATAAACAABTCTTCCGGA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTGGCAACCTGAGTCTATAAACAABTCTTCCGGA 3420  
QY 3421 GTAATTGTAGCATCTCAATAAATAAGCAAGAAATATGAAGAGTTCAGACTGTGA 3480  
|||||

Db 3421 GTAATTGTAGCATCTCAATAAATAAGCAAGAAATATGAAGAGTTCAGACTGTGA 3480  
QY 3481 ATACAGATTTCTCTCCATATTCATTTGATTTAGATTAAGAACAGCCTATGGGAATGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATTCATTTGATTTAGATTAAGAACAGCCTATGGGAATGTC 3540  
QY 3541 ATGCACTCTAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGCTGAATTAAGG 3600  
Db 3541 ATGCACTCTAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGCTGAATTAAGG 3600  
QY 3601 AAGATCTAGTTTGTCTGTAATGACATTAAGGAAGTTTGTGTTTAAAGAAAGCG 3660  
Db 3601 AAGATCTAGTTTGTCTGTAATGACATTAAGGAAGTTTGTGTTTAAAGAAAGCG 3660  
QY 3661 TCCAGAAAGAGAGCTTTAGCAGAGAGTCTAGCCCTTACCCATACACATTTGGCTCAGG 3720  
Db 3661 TCCAGAAAGAGAGCTTTAGCAGAGAGTCTAGCCCTTACCCATACACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGTCTCTCAGAAAGAACCTTATCTAGTAGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGTCTCTCAGAAAGAACCTTATCTAGTAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAAACAATATACCTTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAAACAATATACCTTCAGT 3840  
QY 3841 CTAATAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900  
Db 3841 CTAATAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900  
QY 3901 TATCATGGAAGATAGCTTAATATGATGCTAGTAACACAGTAAATTTGGCAAGGACATCTC 3960  
Db 3901 TATCATGGAAGATAGCTTAATATGATGCTAGTAACACAGTAAATTTGGCAAGGACATCTC 3960  
QY 3961 AGGAACATCACCTTATGAGGAAAGAAACAAATGTTCTGCTAGGCTTGTCTTCCACAGTGA 4020  
Db 3961 AGGAACATCACCTTATGAGGAAAGAAACAAATGTTCTGCTAGGCTTGTCTTCCACAGTGA 4020  
QY 4021 GTGAATTTGGAAGACTTGACTGCAATTAACAAACCCAGAGATCTTCTGTAATGGTCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGACTGCAATTAACAAACCCAGAGATCTTCTGTAATGGTCTT 4080  
QY 4081 CCAAAACAATGAGGATGATGCTGAAAGCCAGGGGTTGGTCTGAGTGAACAAGGAATGG 4140  
Db 4081 CCAAAACAATGAGGATGATGCTGAAAGCCAGGGGTTGGTCTGAGTGAACAAGGAATGG 4140  
QY 4141 TTTCAATGATGATGAAGAAAGAGGAAAGGCGCTTGAAGAAATTAATCAAGAGCAAGCA 4200  
Db 4141 TTTCAATGATGATGAAGAAAGAGGAAAGGCGCTTGAAGAAATTAATCAAGAGCAAGCA 4200  
QY 4201 TGGATTTCAAACTTAAAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAACCGCTCTGAAG 4260  
Db 4201 TGGATTTCAAACTTAAAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAACCGCTCTGAAG 4260  
QY 4261 ACTGCTCAGGGGTATCCCTCTCAGAGTGCATTTTAACCTCACACAGAGGATTAACATGC 4320  
Db 4261 ACTGCTCAGGGGTATCCCTCTCAGAGTGCATTTTAACCTCACACAGAGGATTAACATGC 4320  
QY 4321 AACATTAACCTGATTAAGTCTCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGAACAGC 4380  
Db 4321 AACATTAACCTGATTAAGTCTCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGAACAGC 4380  
QY 4381 ATGGAGCCAGGCTTCTAACAGCTACCCCTTCATCATTAAGTACTCTTGCCTTGAGG 4440  
Db 4381 ATGGAGCCAGGCTTCTAACAGCTACCCCTTCATCATTAAGTACTCTTGCCTTGAGG 4440  
QY 4441 ACCTGCGAAATCCAGAAAGAGCAATCAGAAAGAGAGTCTTAACTTCCACAGAAAGTA 4500  
Db 4441 ACCTGCGAAATCCAGAAAGAGCAATCAGAAAGAGAGTCTTAACTTCCACAGAAAGTA 4500  
QY 4501 GTGAATTAACCTATTAAGCAGAGATCCAGAAAGGCTTTTGTGCAACAATTTGAGGTGCTG 4560  
Db 4501 GTGAATTAACCTATTAAGCAGAGATCCAGAAAGGCTTTTGTGCAACAATTTGAGGTGCTG 4560



QY 4561 CAGATAGTCTACCACTAAATAAAGAACAGAGTGGAAAGTCAATCCCTTCTTAAT 4520  
 |||||||  
 Db 4561 CAGATAGTCTACCACTAAATAAAGAACAGAGTGGAAAGTCAATCCCTTCTTAAT 4520  
 QY 4621 GCCATCATATAGATGATGAGTGGTACATGCACAGTTGCTGGGAGTCTCAGAAATGAA 4680  
 |||||||  
 Db 4621 GCCATCATATAGATGATGAGTGGTACATGCACAGTTGCTGGGAGTCTCAGAAATGAA 4680  
 QY 4681 ACTACCATCTCAAGAGAGAGCTCATTAAGGTTGTGATGTGAGAGCAACAGCTGGAG 4740  
 |||||||  
 Db 4681 ACTACCATCTCAAGAGAGAGCTCATTAAGGTTGTGATGTGAGAGCAACAGCTGGAG 4740  
 QY 4741 AGCTGGGGCCACACGATTTTACGGAAACATCTTACTTCCCAAGCAGATCTAGAGGAA 4800  
 |||||||  
 Db 4741 AGCTGGGGCCACACGATTTTACGGAAACATCTTACTTCCCAAGCAGATCTAGAGGAA 4800  
 QY 4801 CCCCTTACCTGGAATCGAATCAGCCCTTCTCTGATGACCTGAAATCTGATCCCTCTG 4860  
 |||||||  
 Db 4801 CCCCTTACCTGGAATCGAATCAGCCCTTCTCTGATGACCTGAAATCTGATCCCTCTG 4860  
 QY 4861 AAGACAGAGCCCCAGAGTCAAGTCTGTTGGCAACATACCATCTTCAACCTCTGCATGA 4920  
 |||||||  
 Db 4861 AAGACAGAGCCCCAGAGTCAAGTCTGTTGGCAACATACCATCTTCAACCTCTGCATGA 4920  
 QY 4921 AAGTCCCAATGAAAGTTCGAGAAATCTGCCAGAGTCCAGTGCCTGCTCATACTG 4980  
 |||||||  
 Db 4921 AAGTCCCAATGAAAGTTCGAGAAATCTGCCAGAGTCCAGTGCCTGCTCATACTG 4980  
 QY 4981 ATACTGCTGGGTAAATGCAATGGAAGAAAGTGTGAGCAGAGGAGAAAGCAGAAATGACAG 5040  
 |||||||  
 Db 4981 ATACTGCTGGGTAAATGCAATGGAAGAAAGTGTGAGCAGAGGAGAAAGCAGAAATGACAG 5040  
 QY 5041 CTTCACAGAAAGGGTCAACAAAGAAATGTCATGCTGTGCTGGCCTGACCCAGAG 5100  
 |||||||  
 Db 5041 CTTCACAGAAAGGGTCAACAAAGAAATGTCATGCTGTGCTGGCCTGACCCAGAG 5100  
 QY 5101 AATTATGCTCGTGTACAAATTTGCCAGAAACCAACATCATCTTACTTAATTA 5160  
 |||||||  
 Db 5101 AATTATGCTCGTGTACAAATTTGCCAGAAACCAACATCATCTTACTTAATTA 5160  
 QY 5161 CTGAAGAGACTACTCATGTTGTATGAAAACAGATGCTGAGTTGTGTGAACGGAC 5220  
 |||||||  
 Db 5161 CTGAAGAGACTACTCATGTTGTATGAAAACAGATGCTGAGTTGTGTGAACGGAC 5220  
 QY 5221 TGAATATTTTCTAGGAATTCGCGAGGAAATGGTATGTTAGCTATTTCTGGGTGACC 5280  
 |||||||  
 Db 5221 TGAATATTTTCTAGGAATTCGCGAGGAAATGGTATGTTAGCTATTTCTGGGTGACC 5280  
 QY 5281 AGCTATTTAAAGAAAGAAATCTGTAATGAGTATTTTGAAGTCAGAGGAGATGTG 5340  
 |||||||  
 Db 5281 AGCTATTTAAAGAAAGAAATCTGTAATGAGTATTTTGAAGTCAGAGGAGATGTG 5340  
 QY 5341 TCATATGGAAGAAACCAAGGTCCAAGGAGCAGAGAAATCCAGAGAGAGAAAGTCT 5400  
 |||||||  
 Db 5341 TCATATGGAAGAAACCAAGGTCCAAGGAGCAGAGAAATCCAGAGAGAGAAAGTCT 5400  
 QY 5401 TCAGGGGGGTAGAAATCTGTTGCTATGGCCCTTCAACCAATGCCCAAGATCAATGG 5460  
 |||||||  
 Db 5401 TCAGGGGGGTAGAAATCTGTTGCTATGGCCCTTCAACCAATGCCCAAGATCAATGG 5460  
 QY 5461 AATGATGATGACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTTCAATCAATCCCTTG 5520  
 |||||||  
 Db 5461 AATGATGATGACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTTCAATCAATCCCTTG 5520  
 QY 5521 GCACAGGTGTCACCAATGTGTGTGTCAGGACAGATGCTGAGAGAGACAAATGGCT 5580  
 |||||||  
 Db 5521 GCACAGGTGTCACCAATGTGTGTGTCAGGACAGATGCTGAGAGAGACAAATGGCT 5580  
 QY 5581 TCATGCAATTTGGGAGAGATGTGTGAGGACACCTGTGGTGACCCGAGAGTGGGTGTGGACA 5640  
 |||||||  
 Db 5581 TCATGCAATTTGGGAGAGATGTGTGAGGACACCTGTGGTGACCCGAGAGTGGGTGTGGACA 5640

QY 5641 GTGTAGCACTCTACGAGTGGAGAGCTGGACACTACCTGATATCCAGATCCCCACA 5700  
 |||||||  
 Db 5641 GTGTAGCACTCTACGAGTGGAGAGCTGGACACTACCTGATATCCAGATCCCCACA 5700  
 QY 5701 GCCACTACTGA 5711  
 |||||||  
 Db 5701 GCCACTACTGA 5711  
 RESULT 3  
 V46463  
 ID V46463 standard; cDNA: 5711 BP.  
 AC V46463;  
 DT 18-NOV-1998 (first entry)  
 DE Human BRCA1 om12 polymorphism #6 cDNA.  
 KW BRCA1; om12; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; s8.  
 OS Homo sapiens.  
 FH Homo sapiens.  
 FT key Location/Qualifiers  
 FT CDS 120..5711  
 FT /tag- a  
 FT /product- "BRCA1 om12 protein"  
 FT variation 4427  
 FT /tag- b  
 FT /note- "This polymorphic variation can be a T or C nucleotide"  
 PN US5750400-A.  
 PD 12-MAY-1998.  
 PF 12-FEB-1997; 798691.  
 PR 12-FEB-1996; US-558591.  
 PR 12-FEB-1997; US-798691.  
 PA (ONCO-) ONCORMED INC.  
 PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,  
 PI Schelter DB, Zeng B;  
 DR WPI: 98-296774/26.  
 PT BRCA1 om1 gene coding sequences - useful for distinguishing between  
 PT polymorphisms and mutation(s) in the screening for disposition to  
 PT breast or ovarian cancer  
 PS Claim 2e; Page -: 54pp; English.  
 CC This sequence encodes a human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) om12 gene in which a polymorphic variation occurs at  
 CC nucleotide 4427. This sequence and other polymorphic variations of this  
 CC sequence are useful for the identification of an individual who may or  
 CC may not have an increased susceptibility to breast or ovarian cancer.  
 CC The sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome 17q  
 CC which is known to be linked to cancer susceptibility, especially breast  
 CC cancer. Cells containing a mutation in this gene lose the wild-type  
 CC function of BRCA1 and are more susceptible to cancers.  
 CC NOTE: This sequence does not appear in the specification but has been  
 CC created from the wild type BRCA1 om12 gene represented in V46449.  
 SQ Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1382 T;  
 Query Match 100.0%; Score 5710.6; DB 1; Length 5711;  
 Best local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTGCTGAGACTCTCTGGACCCGACACAGGCTGTGGGGTTTCTCAGATTAATGGGCC 60  
 |||||||  
 Db 1 AGCTGCTGAGACTCTCTGGACCCGACACAGGCTGTGGGGTTTCTCAGATTAATGGGCC 60  
 QY 61 CCGGCGCTAGAGAGGCTTCAACCTCTGCTGCGTGAAGTTGATGGAACAAGAGAA 120  
 |||||||  
 Db 61 CCGGCGCTAGAGAGGCTTCAACCTCTGCTGCGTGAAGTTGATGGAACAAGAGAA 120  
 QY 121 TGGATTATCTGCTCTTCCGTTGAGAGATCAAAATGCTATTATGCTATGCAGAAAA 180  
 |||||||  
 Db 121 TGGATTATCTGCTCTTCCGTTGAGAGATCAAAATGCTATTATGCTATGCAGAAAA 180

QY 181 TCTTGAAGTGTCCCATCTGTCTGAGAGTGTATCAAGAACTGTCTCCAAAGTGTGACC 240  
DB 181 TCTTGAAGTGTCCCATCTGTCTGAGAGTGTATCAAGAACTGTCTCCAAAGTGTGACC 240  
QY 241 ACATATTTTGGCAATTTTTCATGCTGAAACTTCTCAACCGAAGAAAGGGGCTTCACAGT 300  
DB 241 ACATATTTTGGCAATTTTTCATGCTGAAACTTCTCAACCGAAGAAAGGGGCTTCACAGT 300  
QY 301 GTCCTTATGTAGAATGATATATACCAAAAGAGCCCTACAGAAAGTACAGATTTAGTC 360  
DB 301 GTCCTTATGTAGAATGATATATACCAAAAGAGCCCTACAGAAAGTACAGATTTAGTC 360  
QY 361 AACTTGTTAAGAAGCTATTTGAATAATCATTTGTCTTTTCAAGCTTTGACAGGTTTGGAGT 420  
DB 361 AACTTGTTAAGAAGCTATTTGAATAATCATTTGTCTTTTCAAGCTTTGACAGGTTTGGAGT 420  
QY 421 ATGCAACAGCTATATATTTTGCNAAAAGAAATAACTCTCTGAACATCTAAAAGATG 480  
DB 421 ATGCAACAGCTATATATTTTGCNAAAAGAAATAACTCTCTGAACATCTAAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCNAAAAGACTTCTACAGAGTG 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCNAAAAGACTTCTACAGAGTG 540  
QY 541 AACCCGAAATTCCTTCTCTGAGGAAACAGTCTCAAGTGTCCAACTCTTACCTTGGAA 600  
DB 541 AACCCGAAATTCCTTCTCTGAGGAAACAGTCTCAAGTGTCCAACTCTTACCTTGGAA 600  
QY 601 CTGTGAGAACTCTGAGGAAAGCAGCGATACAACTCTAAAAGAGCTGTCTACATTTG 660  
DB 601 CTGTGAGAACTCTGAGGAAAGCAGCGATACAACTCTAAAAGAGCTGTCTACATTTG 660  
QY 661 AATTTGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCACTTATTTGCAAGTGGGAG 720  
DB 661 AATTTGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCACTTATTTGCAAGTGGGAG 720  
QY 721 ATCAAGAATGTGTACAAATCACCCCTCAAGAAACCAAGGGGTGAATTCAGTTGGATCTG 780  
DB 721 ATCAAGAATGTGTACAAATCACCCCTCAAGAAACCAAGGGGTGAATTCAGTTGGATCTG 780  
QY 781 CAAAAAAGGCTCTGTGTGAATTTTCTGAGACGAGTATACAAATACTGAAATCATCATAC 840  
DB 781 CAAAAAAGGCTCTGTGTGAATTTTCTGAGACGAGTATACAAATACTGAAATCATCATAC 840  
QY 841 CCAGTAATATATATTTGAACACCACTGAGAAAGCTGACAGTGAAGGACATCCGAAAAAGT 900  
DB 841 CCAGTAATATATATTTGAACACCACTGAGAAAGCTGACAGTGAAGGACATCCGAAAAAGT 900  
QY 901 ATCAGGGTATGTCTGTCTTCAAACTGATGTGAGGCAATGTGACACAAATATCATGCCA 960  
DB 901 ATCAGGGTATGTCTGTCTTCAAACTGATGTGAGGCAATGTGACACAAATATCATGCCA 960  
QY 961 GCTCATTCAGCATGAGAACAGAGTTTATTACTCACTAAGACAGATATGATGAAAA 1020  
DB 961 GCTCATTCAGCATGAGAACAGAGTTTATTACTCACTAAGACAGATATGATGAAAA 1020  
QY 1021 AGGCTGAATTTCTGTATATAAAGCAACAGCTGTAGAGAGGAGCCAACTATACAGAT 1080  
DB 1021 AGGCTGAATTTCTGTATATAAAGCAACAGCTGTAGAGAGGAGCCAACTATACAGAT 1080  
QY 1081 GGGGCTGAAGTAAAGAAACATGTATAGTATAGGGGACTCCACAGCAGAAAAAGGTAG 1140  
DB 1081 GGGGCTGAAGTAAAGAAACATGTATAGTATAGGGGACTCCACAGCAGAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGATGGAATAAGCAGAAATCCCATGCT 1200  
DB 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGATGGAATAAGCAGAAATCCCATGCT 1200  
QY 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATTAACACTAAATAGCAGCATTCAGA 1260  
DB 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATTAACACTAAATAGCAGCATTCAGA 1260  
QY 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAAGTGTAGTGTGATGACTCAGATGATG 1320  
DB 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAAGTGTAGTGTGATGACTCAGATGATG 1320  
QY 1321 GGGAGTCTGAATCAATATGCCAAAGTACGATGATTTGGACGTTTCAATAGAGTATG 1380  
DB 1321 GGGAGTCTGAATCAATATGCCAAAGTACGATGATTTGGACGTTTCAATAGAGTATG 1380  
QY 1381 AATATTTCTGTTCTTTCAGAGAAATATGACTTACTGCGCAGTGTCTCATAGGCTTTAA 1440  
DB 1381 AATATTTCTGTTCTTTCAGAGAAATATGACTTACTGCGCAGTGTCTCATAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTATAGAGTAAATTTGAGACAAATAT 1500  
DB 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTATAGAGTAAATTTGAGACAAATAT 1500  
QY 1501 TTGGGAAACCTATTCGGAAGAAAGGCAAGCCTCCCAACTTAAGCCATGTAAGTGA 1560  
DB 1501 TTGGGAAACCTATTCGGAAGAAAGGCAAGCCTCCCAACTTAAGCCATGTAAGTGA 1560  
QY 1561 TAAATTTAGAGCATTTGTTACTGAGCCACAGATTAATACAAAGGCTCCCTCACAAATA 1620  
DB 1561 TAAATTTAGAGCATTTGTTACTGAGCCACAGATTAATACAAAGGCTCCCTCACAAATA 1620  
QY 1621 AATTTAAAGGTTAAAGAGACCTACATCAGGCTTCATCCTGAGATTTTATCAGAAAG 1680  
DB 1621 AATTTAAAGGTTAAAGAGACCTACATCAGGCTTCATCCTGAGATTTTATCAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTTCAAAAGACTCTGTAATGATAAATACGAGAACTAAACCAAGGAGC 1740  
DB 1681 CAGATTTGGCAGTTTCAAAAGACTCTGTAATGATAAATACGAGAACTAAACCAAGGAGC 1740  
QY 1741 AGAATGCTCAAGTATGATATTTACTAATATGCTCATAGAAATTAACAAAGTGAAT 1800  
DB 1741 AGAATGCTCAAGTATGATATTTACTAATATGCTCATAGAAATTAACAAAGTGAAT 1800  
QY 1801 CTATTCAGATGGAATAATTCCTAACCAATAGAAATCACTCCAAAAAGATGTGTTTCA 1860  
DB 1801 CTATTCAGATGGAATAATTCCTAACCAATAGAAATCACTCCAAAAAGATGTGTTTCA 1860  
QY 1861 AAACGAAAGCTGAACCTATATAGCAGCATATAGCAATATGAGAACTGCAATTAATATCC 1920  
DB 1861 AAACGAAAGCTGAACCTATATAGCAGCATATAGCAATATGAGAACTGCAATTAATATCC 1920  
QY 1921 ACAATTTCAAAAGCACTTAATAAAGATATAGCTGAGAGAAAGTCTTACAGGCAATATTC 1980  
DB 1921 ACAATTTCAAAAGCACTTAATAAAGATATAGCTGAGAGAAAGTCTTACAGGCAATATTC 1980  
QY 1981 ATGCGCTGAACTAGTATGATCAGTAAATCTTAAGCCCACTTAATGTACTGAATTTGCAAA 2040  
DB 1981 ATGCGCTGAACTAGTATGATCAGTAAATCTTAAGCCCACTTAATGTACTGAATTTGCAAA 2040  
QY 2041 TTGATAGTTGTTCTAGCACTGAGAGATTAAGAAAAAGTATCAACCAATATGCCAGTCA 2100  
DB 2041 TTGATAGTTGTTCTAGCACTGAGAGATTAAGAAAAAGTATCAACCAATATGCCAGTCA 2100  
QY 2101 GGCACAGCAGAAACCTTACAACTCATGGAAGGTAAAGAACTCAACTGAGGCCAAGAAAG 2160  
DB 2101 GGCACAGCAGAAACCTTACAACTCATGGAAGGTAAAGAACTCAACTGAGGCCAAGAAAG 2160  
QY 2161 GTAAACAGCCAAATGAAAGACAGAAAGTAAAGACATGACAGGCAATCTTTCCAGAGCTGA 2220  
DB 2161 GTAAACAGCCAAATGAAAGACAGAAAGTAAAGACATGACAGGCAATCTTTCCAGAGCTGA 2220  
QY 2221 AGTTAACAATGCACTGTCTTTTACTAATGTTTCAATACAGTAACTTAAGAT 2280  
DB 2221 AGTTAACAATGCACTGTCTTTTACTAATGTTTCAATACAGTAACTTAAGAT 2280  
QY 2281 TTGTCAATCTTACCTTCCAAAGAGAAAGAAAGAACTACAAACAGTTAAAGTGT 2340  
DB 2281 TTGTCAATCTTACCTTCCAAAGAGAAAGAAAGAAAGAACTACAAACAGTTAAAGTGT 2340  
QY 2341 CTATATATGCTAAAGAGCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCAAATG 2400  
DB 2341 CTATATATGCTAAAGAGCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCAAATG 2400

Db 2341 CTAATATGCTGAGAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGCTTTGCAACTG 2400  
QY 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCTATTGTAAGTCTGGTACTGATTAATGCACTCAGG 2460  
Db 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCTATTGTAAGTCTGGTACTGATTAATGCACTCAGG 2460  
QY 2461 AAAGATCTGTCTACTGTAGAGAGTAGCAGTATTTCTATTGTAAGTCTGGTACTGATTAAT 2520  
Db 2461 AAAGATCTGTCTACTGTAGAGAGTAGCAGTATTTCTATTGTAAGTCTGGTACTGATTAAT 2520  
QY 2521 GTGTAGTCAAGTGTGACAGTATTTGAAACCCCAAGGAGTAAATTCATGTTGTTCCAAAG 2580  
Db 2521 GTGTAGTCAAGTGTGACAGTATTTGAAACCCCAAGGAGTAAATTCATGTTGTTCCAAAG 2580  
QY 2581 ATTAATAGAAATGACACAGAGGCTTTAAGTATTCATTTGGGACATGAAGTTAAACCAAGTTC 2640  
Db 2581 ATTAATAGAAATGACACAGAGGCTTTAAGTATTCATTTGGGACATGAAGTTAAACCAAGTTC 2640  
QY 2641 GGGAAACAGAGATAGAAATGGAAGAAAGTGAAGTGTGATGCTCAGTATTTGCAAGAAATAT 2700  
Db 2641 GGGAAACAGAGATAGAAATGGAAGAAAGTGAAGTGTGATGCTCAGTATTTGCAAGAAATAT 2700  
QY 2701 TCAAGGTTTCAAGAGGCGGAGTCTATTTGCTGTTTCAAAATCCAGGAATGAGAGAGG 2760  
Db 2701 TCAAGGTTTCAAGAGGCGGAGTCTATTTGCTGTTTCAAAATCCAGGAATGAGAGAGG 2760  
QY 2761 AATGTGCAACATTTCTGCTGCGCCACTGCTGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCTGCGCCACTGCTGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGGAAGATGAGTCTTAATTCAGGCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGGAAGATGAGTCTTAATTCAGGCTGTAC 2880  
QY 2881 AGACAGTAAATATCATCTCAGGCTTCTGCTGTGTGTGTCAGAGAAATAGCAGAGTTGATA 2940  
Db 2881 AGACAGTAAATATCATCTCAGGCTTCTGCTGTGTGTGTCAGAGAAATAGCAGAGTTGATA 2940  
QY 2941 ATGCCAAATGTAGATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA 3000  
Db 2941 ATGCCAAATGTAGATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA 3000  
QY 3001 ACGAAACTGAGCTCATTTCTCCAAATAAACAATGACCTTTTACAAAACCCATATGCTATAC 3060  
Db 3001 ACGAAACTGAGCTCATTTCTCCAAATAAACAATGACCTTTTACAAAACCCATATGCTATAC 3060  
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAATGTAAAGAAATGCTGTAGAGG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAATGTAAAGAAATGCTGTAGAGG 3120  
QY 3121 AAAACTTTGAGGAACATTCATTCACCTGAAAGAAATGGGAATGAGAACATTTCCAA 3180  
Db 3121 AAAACTTTGAGGAACATTCATTCACCTGAAAGAAATGGGAATGAGAACATTTCCAA 3180  
QY 3181 GTACAGTAGAGACATTTAGCCGTATATACATTAAGAGAAAGTTTTAAAGAGCCACT 3240  
Db 3181 GTACAGTAGAGACATTTAGCCGTATATACATTAAGAGAAAGTTTTAAAGAGCCACT 3240  
QY 3241 CAAGCAATATTAATGAAGTAGTTCACATTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGTTCACATTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
QY 3301 TAGGTTCCAGTATGAAGAAACATTCAGAGAGAACTAGTGAAGAACAGAGGCCAAATATGA 3360  
Db 3301 TAGGTTCCAGTATGAAGAAACATTCAGAGAGAACTAGTGAAGAACAGAGGCCAAATATGA 3360  
QY 3361 ATGCTATGCTAGANTTAGGGTTTTGCAACCTGAGGCTATATTAACAAAGTCTTCTGAAA 3420  
Db 3361 ATGCTATGCTAGANTTAGGGTTTTGCAACCTGAGGCTATATTAACAAAGTCTTCTGAAA 3420  
QY 3421 GTAATTGTAAACATCTGAAATTAAGAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTTA 3480  
Db 3421 GTAATTGTAAACATCTGAAATTAAGAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTTA 3480

QY 3481 ATACAGATTTCTCTCCATATCTGATTTACATTAATCTAGAAACAGCCTATGAGGAATGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTACATTAATCTAGAAACAGCCTATGAGGAATGTC 3540  
QY 3541 ATGATCTCAGGTTGTGTTCTGAGACACCTGATGACCTGTTAGATGATGTAATTAAGG 3600  
Db 3541 ATGATCTCAGGTTGTGTTCTGAGACACCTGATGACCTGTTAGATGATGTAATTAAGG 3600  
QY 3601 AAGTACTAGTTTGTGGAATAATGACATTAAGAAAGTTCGCTGTTTAAAGCAAAAGCG 3660  
Db 3601 AAGTACTAGTTTGTGGAATAATGACATTAAGAAAGTTCGCTGTTTAAAGCAAAAGCG 3660  
QY 3661 TCCAGAAAGAGACCTTAGCAGAGTCCCTAGCCTTCCACCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAAAGAGACCTTAGCAGAGTCCCTAGCCTTCCACCATACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGGGGGCCCAAGAAATTAAGATCCTAGAGAAAGAACTTAATCTGTAGAGATG 3780  
Db 3721 GTTACCGAAGGGGGCCCAAGAAATTAAGATCCTAGAGAAAGAACTTAATCTGTAGAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTCCACACTTGTATTTGTTAAAGTAAACAAATATACCTTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTCCACACTTGTATTTGTTAAAGTAAACAAATATACCTTCAGT 3840  
QY 3841 CTACTAGGCAATAGCACCCTGTGCTACGAGTGTCTGTAAAGACACAGAGAGAAATTAAT 3900  
Db 3841 CTACTAGGCAATAGCACCCTGTGCTACGAGTGTCTGTAAAGACACAGAGAGAAATTAAT 3900  
QY 3901 TATCATTTGAAGAAATAGCTTTAATATCTGACATACACAGGTAATTTGGCAAGGCACTTC 3960  
Db 3901 TATCATTTGAAGAAATAGCTTTAATATCTGACATACACAGGTAATTTGGCAAGGCACTTC 3960  
QY 3961 AGGAACATCATCTTAGTAGAGAAACAAATTTCTGATAGCTTGTCTTCAAGTGA 4020  
Db 3961 AGGAACATCATCTTAGTAGAGAAACAAATTTCTGATAGCTTGTCTTCAAGTGA 4020  
QY 4021 GTGAATTTGAAGACTTGATGATCAATTAACAAACACCCAGAGATCTTCTGTAGTGTCTT 4080  
Db 4021 GTGAATTTGAAGACTTGATGATCAATTAACAAACACCCAGAGATCTTCTGTAGTGTCTT 4080  
QY 4081 CCAACCAATGAGGATCAAGTCTGAAGCCGAGAGTGGCTGATGAGACAAAGAAATGG 4140  
Db 4081 CCAACCAATGAGGATCAAGTCTGAAGCCGAGAGTGGCTGATGAGACAAAGAAATGG 4140  
QY 4141 TTTGAGATGATGAAGAAAGAGGAGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200  
Db 4141 TTTGAGATGATGAAGAAAGAGGAGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200  
QY 4201 TGGATTCAAACTTAGTGAAGCAGCATCTGGGTGTGAAGTGAAGCAAGCGTCTCTGAAG 4260  
Db 4201 TGGATTCAAACTTAGTGAAGCAGCATCTGGGTGTGAAGTGAAGCAAGCGTCTCTGAAG 4260  
QY 4261 ACTGCTCAGGCTATCTCTGAGATGACATTTTAAACCACTCAGACAGAGGATACCATGC 4320  
Db 4261 ACTGCTCAGGCTATCTCTGAGATGACATTTTAAACCACTCAGACAGAGGATACCATGC 4320  
QY 4321 AACATTAACCTGATTAACCTCCAGCAGAAATGCTGAACCTGGAAGCTGTGTTAAACAGC 4380  
Db 4321 AACATTAACCTGATTAACCTCCAGCAGAAATGCTGAACCTGGAAGCTGTGTTAAACAGC 4380  
QY 4381 ATGGAGCCAGCCTTCTTAACAGCTACCTTCATCATATGAGTACTCTTCCCTGAGG 4440  
Db 4381 ATGGAGCCAGCCTTCTTAACAGCTACCTTCATCATATGAGTACTCTTCCCTGAGG 4440  
QY 4441 ACCGCGCAAAATCCAGAACAAAGCAGATCAGAAAGAGATTAATCTTCCAGAAAGTA 4500  
Db 4441 ACCGCGCAAAATCCAGAACAAAGCAGATCAGAAAGAGATTAATCTTCCAGAAAGTA 4500  
QY 4501 GTGAATACCCCTATTAAGCCAGATATCAGAAAGGCTTCTGTGACAAATTTGAGGCTGTG 4560  
Db 4501 GTGAATACCCCTATTAAGCCAGATATCAGAAAGGCTTCTGTGACAAATTTGAGGCTGTG 4560



```
Db 181 TCTTGAAGTGTCCCATCTGTCTGGAGTTGATCAGAACTCTGTCCCAAGTGTGACC 240
Qy 241 ACAATTTTGGCAAAATTTTGGCATGCTGAAACCTTCTCACAGAGAAAGGGCCCTCACAGT 300
Db 241 ACAATTTTGGCAAAATTTTGGCATGCTGAAACCTTCTCACAGAGAAAGGGCCCTCACAGT 300
Qy 301 GTCCCTTTATGTAAGATATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTACTC 360
Db 301 GTCCCTTTATGTAAGATATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTACTC 360
Qy 361 AACTGTGGAAGAGCTATGAAATCATTTGCTTTACAGTTGACAGAGTTTGGAGT 420
Db 361 AACTGTGGAAGAGCTATGAAATCATTTGCTTTACAGTTGACAGAGTTTGGAGT 420
Qy 421 ATGCAAAACAGCTATATTTTGCAGAAAGAAATMACTCTCTGMACTGTAAAGATG 480
Db 421 ATGCAAAACAGCTATATATTTTGCAGAAAGAAATMACTCTCTGMACTGTAAAGATG 480
Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAAGACTTTACAGAGTG 540
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAAGACTTTACAGAGTG 540
Qy 541 AACCAGAAATCTCTCTCTTGCAGAGAAACAGTCTAGTGTCCAACTCTTAACCTGGAA 600
Db 541 AACCAGAAATCTCTCTCTTGCAGAGAAACAGTCTAGTGTCCAACTCTTAACCTGGAA 600
Qy 601 CTGTGAGAACTCTGAGAGCAAGCAGCGGATACAACCTCAAAAGAGCTGTCTACATTTG 660
Db 601 CTGTGAGAACTCTGAGAGCAAGCAGCGGATACAACCTCAAAAGAGCTGTCTACATTTG 660
Qy 661 AATTGGGATCTGATTTCTTCTGAAGTACCGTTAATTAAGCAACTTATTCAGTGTGGAG 720
Db 661 AATTGGGATCTGATTTCTTCTGAAGTACCGTTAATTAAGCAACTTATTCAGTGTGGAG 720
Qy 721 ATCAAGAAATTTGTACAAATCAACCCCTCAAGAGCAACGAGGATGAATCAGTTGGATTCTG 780
Db 721 ATCAAGAAATTTGTACAAATCAACCCCTCAAGAGCAACGAGGATGAATCAGTTGGATTCTG 780
Qy 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGTAAACAATACTGACATCATCAAC 840
Db 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGTAAACAATACTGACATCATCAAC 840
Qy 841 CCAGTAATTAATGATTTTGAACACACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAAGT 900
Db 841 CCAGTAATTAATGATTTTGAACACACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAAGT 900
Qy 901 ATCAGGGATGTTGTTTCAAACTGATGAGAGGAGCATGTGGGCAAAATCTCATGCGCA 960
Db 901 ATCAGGGATGTTGTTTCAAACTGATGAGAGGAGCATGTGGGCAAAATCTCATGCGCA 960
Qy 961 GCTCATTAACAGCATGAGAAACAGAGTTTATTACTACTAAAGAGAGATGAATGAGAAA 1020
Db 961 GCTCATTAACAGCATGAGAAACAGAGTTTATTACTACTAAAGAGAGATGAATGAGAAA 1020
Qy 1021 AGGCTGAATTTCTGTAATTAAGCAAAACGCTGCTTGAAGAGGAGCCAACTAACAAT 1080
Db 1021 AGGCTGAATTTCTGTAATTAAGCAAAACGCTGCTTGAAGAGGAGCCAACTAACAAT 1080
Qy 1081 GGGCTGGAAGTAAGGAACATGTAATGATAGGCGGAGCTCCAGCAGAGAAAAGGATG 1140
Db 1081 GGGCTGGAAGTAAGGAACATGTAATGATAGGCGGAGCTCCAGCAGAGAAAAGGATG 1140
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATGAGAGAACTGCGCATCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATGAGAGAACTGCGCATCT 1200
Qy 1201 CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGATTAACCTAATATGCAAGCATTCAGA 1260
Db 1201 CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGATTAACCTAATATGCAAGCATTCAGA 1260
Qy 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATGTTAGTTCTGATACACATGATG 1320
Db 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATGACTGTTAGTTCTGATACACATGATG 1320
Qy 1321 GGAAGTCTGAATCAAAATGCCAAAGTACTGATGATTGAGAGCTTCAATAGGTAGATG 1380
Db 1321 GGAAGTCTGAATCAAAATGCCAAAGTACTGATGATTGAGAGCTTCAATAGGTAGATG 1380
Qy 1381 AATTTCTGCTTCTTCAGAGAAATTAAGTACTACGCGCAGAGATCCATAGAGCTTTAA 1440
Db 1381 AATTTCTGCTTCTTCAGAGAAATTAAGTACTACGCGCAGAGATCCATAGAGCTTTAA 1440
Qy 1441 TATGTAAAGAGAAAGTGTACTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAATAT 1500
Db 1441 TATGTAAAGAGAAAGTGTACTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAATAT 1500
Qy 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAAGTAAATC 1560
Db 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCCATGTAAGTAAATC 1560
Qy 1561 TAAATTATGAGAGCATTTGTTACTGAGCCACAGATATATCAAGAGAGCTCCCTCAATA 1620
Db 1561 TAAATTATGAGAGCATTTGTTACTGAGCCACAGATATATCAAGAGAGCTCCCTCAATA 1620
Qy 1621 AATTAAAGCGTAAAGAGAGACTACATCAGGCTTCAATCTGAGAGATTTTATCAAGAAAG 1680
Db 1621 AATTAAAGCGTAAAGAGAGACTACATCAGGCTTCAATCTGAGAGATTTTATCAAGAAAG 1680
Qy 1681 CAGATTTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGGAAGTAAACCAACGAGC 1740
Db 1681 CAGATTTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGGAAGTAAACCAACGAGC 1740
Qy 1741 AGAATGGCAAGTATGAAATTTTACTAATAGTGTCAATGAGATTAATTAAGGATGTT 1800
Db 1741 AGAATGGCAAGTATGAAATTTTACTAATAGTGTCAATGAGATTAATTAAGGATGTT 1800
Qy 1801 CTATTGAAATGAGAAAAATCTTAACCAATGAGATACCTGAAAGAAATCTGCTTCA 1860
Db 1801 CTATTGAAATGAGAAAAATCTTAACCAATGAGATACCTGAAAGAAATCTGCTTCA 1860
Qy 1861 AAACGAAAGCTGAACCTATAAGAGAGAGTATAGCAATATGAGAACTCGAATTAATATCC 1920
Db 1861 AAACGAAAGCTGAACCTATAAGAGAGAGTATAGCAATATGAGAACTCGAATTAATATCC 1920
Qy 1921 ACAATTTCAAAAGCACCTTAAGAAATAGGCTGAGAGAGAGTCTTCTACCGGATATTC 1980
Db 1921 ACAATTTCAAAAGCACCTTAAGAAATAGGCTGAGAGAGAGTCTTCTACCGGATATTC 1980
Qy 1981 ATGGCGTTGAAGCTAGTGTGTGTAAGAAATCTAAGCCACCTAATTTGTAAGTGAAGA 2040
Db 1981 ATGGCGTTGAAGCTAGTGTGTGTAAGAAATCTAAGCCACCTAATTTGTAAGTGAAGA 2040
Qy 2041 TTGATAGTGTGTTCTAGAGAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGCGAGTCA 2100
Db 2041 TTGATAGTGTGTTCTAGAGAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATGCGAGTCA 2100
Qy 2101 GGCACAGCAGAAACCTTACACTCATGGAAGTAAAGAACTGCAACTGAGGCCAAGAGA 2160
Db 2101 GGCACAGCAGAAACCTTACACTCATGGAAGTAAAGAACTGCAACTGAGGCCAAGAGA 2160
Qy 2161 GTAACAGGCCAAATGAAGACAGAGTAAAGACATGACAGAGAGTCTTCCAGAGCTGA 2220
Db 2161 GTAACAGGCCAAATGAAGACAGAGTAAAGACATGACAGAGAGTCTTCCAGAGCTGA 2220
Qy 2221 AGTTAACAATGACACTGTGTTCTTTACTAAGTGTCAAAATACCAAGGAATCTTAAAGAT 2280
Db 2221 AGTTAACAATGACACTGTGTTCTTTACTAAGTGTCAAAATACCAAGGAATCTTAAAGAT 2280
Qy 2281 TTGTCAATCTTACGCTTCCAGAGAGAGAAAGAAAGAACTTGAAGAGTAAAGTGT 2340
Db 2281 TTGTCAATCTTACGCTTCCAGAGAGAGAAAGAAAGAAAGAACTTGAAGAGTAAAGTGT 2340
Qy 2341 CTAATTAATGCTGAAGAGCCCAAGATCTCATGTTAATGAGAGAAAGGTTTGGAAACTG 2400
Db 2341 CTAATTAATGCTGAAGAGCCCAAGATCTCATGTTAATGAGAGAAAGGTTTGGAAACTG 2400
```



QY	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCATTGTGTAAGCTGTACTGTACTGATTAATGCGACTGAGG	2460
DB	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCATTGTGTAAGCTGTACTGTACTGATTAATGCGACTGAGG	2460
QY	2461	AAAGTATCTGTTACTGTGGAAAGTGTGCACTCTAGGGAAAGGCAAAAACAGAACCAATAAT	2520
DB	2461	AAAGTATCTGTTACTGTGGAAAGTGTGCACTCTAGGGAAAGGCAAAAACAGAACCAATAAT	2520
QY	2521	GTGTGATCTCAGTGTGCAAGCATTTTGAAAAACCCCAAGGGCACTAATTCATAGTTGTTCGAAG	2580
DB	2521	GTGTGATCTCAGTGTGCAAGCATTTTGAAAAACCCCAAGGGCACTAATTCATAGTTGTTCGAAG	2580
QY	2581	ATAATAGAAAATGACACAGAAAGGCTTTAAGTATCCATTGGACATGAAGTTAACCACAGTC	2640
DB	2581	ATAATAGAAAATGACACAGAAAGGCTTTAAGTATCCATTGGACATGAAGTTAACCACAGTC	2640
QY	2641	GGGAACACACATTAAGAAATGGAGAAAGTGAACTTGATGCTCAGTATTTGCAATTCAT	2700
DB	2641	GGGAACACACATTAAGAAATGGAGAAAGTGAACTTGATGCTCAGTATTTGCAATTCAT	2700
QY	2701	TCAGGCTTTCAAAAGCCGCACTATTGTGCTGTGTTTCAAAATCCAGGAAAGACAAAGAGG	2760
DB	2701	TCAGGCTTTCAAAAGCCGCACTATTGTGCTGTGTTTCAAAATCCAGGAAAGACAAAGAGG	2760
QY	2761	AATGTGCACATTTCTCTGCCACCTGTGGGTCTTTAAAGAAACAAGTCCAAAGTCACTT	2820
DB	2761	AATGTGCACATTTCTCTGCCACCTGTGGGTCTTTAAAGAAACAAGTCCAAAGTCACTT	2820
QY	2821	TTTAATGTGACACAAAGGAAGAAATTAAGGAAAGATGAGCTTAATATCAAGCTGTAC	2880
DB	2821	TTTAATGTGACACAAAGGAAGAAATTAAGGAAAGATGAGCTTAATATCAAGCTGTAC	2880
QY	2881	AGACAGTTAATATCAGCTGCAGGCTTTCCTGTGTTGTTGTCAGAAAGATTAAGCAGTTGATA	2940
DB	2881	AGACAGTTAATATCAGCTGCAGGCTTTCCTGTGTTGTTGTTGTCAGAAAGATTAAGCAGTTGATA	2940
QY	2941	ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCACTCAGTCAAGAGCA	3000
DB	2941	ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCACTCAGTCAAGAGCA	3000
QY	3001	ACGAACCTGCACATTTACTCCCAATTAATATGAGACTTTTACAAAACCCATATCGTATAC	3060
DB	3001	ACGAACCTGCACATTTACTCCCAATTAATATGAGACTTTTACAAAACCCATATCGTATAC	3060
QY	3061	CACCACTTTTCCCATCAAGTCAATTGTGTTAAACTAAATGTAGAAGAAAATCTGTGAGG	3120
DB	3061	CACCACTTTTCCCATCAAGTCAATTGTGTTAAACTAAATGTAGAAGAAAATCTGTGAGG	3120
QY	3121	AAAACCTTGAAGGAACATTCATGTCACTGACCTGAAAGAGAAATGGGAAATGAGACATTCGAA	3180
DB	3121	AAAACCTTGAAGGAACATTCATGTCACTGACCTGAAAGAGAAATGGGAAATGAGACATTCGAA	3180
QY	3181	GTACAGTGTGACACATTTAGCCGTAAATATACATTAGAGAAAAATGTTTTTAAAGAACCAAGCT	3240
DB	3181	GTACAGTGTGACACAAATTTAGCCGTAAATATACATTAGAGAAAAATGTTTTTAAAGAACCAAGCT	3240
QY	3241	CAAGCAATTTATGAAGTAGAGTTCCAGTACTATGAATGAAGGGGCTCCAGATTAATAGAAA	3300
DB	3241	CAAGCAATTTATGAAGTAGAGTTCCAGTACTATGAATGAAGGGGCTCCAGATTAATAGAAA	3300
QY	3301	TAGGTTCCAGTGTGAAAAATTCAGAGACAGACATTCAGAGAACAGAGGGCCAAAATTTGA	3360
DB	3301	TAGGTTCCAGTGTGAAAAATTCAGAGACAGACATTCAGAGAACAGAGGGCCAAAATTTGA	3360
QY	3361	ATGCTATGCTTATGATTAGGGGTTTGCAAACCTGAGGTCATATAACAAAGTCTTCTGGA	3420
DB	3361	ATGCTATGCTTATGATTAGGGGTTTGCAAACCTGAGGTCATATAACAAAGTCTTCTGGA	3420
QY	3421	GTAAATTTGTAAGATCCTGAAATTAATAAACAAGAAATATGAGAAAGTAGTTCAAGCTGTA	3480
DB	3421	GTAAATTTGTAAGATCCTGAAATTAATAAACAAGAAATATGAGAAAGTAGTTCAAGCTGTA	3480

QY	3481	ATACGAGATTTCCTCCCATATCTGATTTCAGATTAACCTTAGACACGCTATGGGAAGTAGTC	3544
Db	3481	ATACGAGATTTCCTCCCATATCTGATTTCAGATTAACCTTAGACACGCTATGGGAAGTAGTC	3544
QY	3541	ATGCATCTCAGGTTGTTCTGAGACACCTGATGCCGTTAGATGATGGTGAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTGTTCTGAGACACCTGATGCCGTTAGATGATGGTGAATTAAGG	3600
QY	3601	AAGATACAGTTTTGCTGTAATAATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAAGCG	3660
Db	3601	AAGATACAGTTTTGCTGTAATAATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAAGCG	3660
QY	3661	TCCAAAAAGAGAGCTTAGACAGAGTCTTAGCCCTTACACCATACACTTTGGCTCAGG	3720
Db	3661	TCCAAAAAGAGAGCTTAGACAGAGTCTTAGCCCTTACACCATACACTTTGGCTCAGG	3720
QY	3721	GTTACCGAAGAGGGGCCAAGAAATTAAGTCTCAGAAAGAACTTATCTAGAGAGATG	3780
Db	3721	GTTACCGAAGAGGGGCCAAGAAATTAAGTCTCAGAAAGAACTTATCTAGAGAGATG	3780
QY	3781	AAGAGCTTCCTGCTCCCAACACTGTTATTTGGTAAAGTAAACAATATACCTTCAGT	3840
Db	3781	AAGAGCTTCCTGCTCCCAACACTGTTATTTGGTAAAGTAAACAATATACCTTCAGT	3840
QY	3841	CTACTAGGCATAGCACCGCTGCTACCGAGTGTGTCATAAGAACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCATAGCACCGCTGCTACCGAGTGTGTCATAAGAACACAGAGAGAAATTTAT	3900
QY	3901	TATCATTTGAAGAAATAGGTTAAATGACTCGCAGTAAACCAAGTATATTTGGCAAGGATCTC	3960
Db	3901	TATCATTTGAAGAAATAGGTTAAATGACTCGCAGTAAACCAAGTATATTTGGCAAGGATCTC	3960
QY	3961	AGGAACATCACCTTAGAGAGAGAAACAAAATGTTCTGCTAGCTTTGTTCTTCACAGTCA	4020
Db	3961	AGGAACATCACCTTAGAGAGAGAAACAAAATGTTCTGCTAGCTTTGTTCTTCACAGTCA	4020
QY	4021	GTTGAATTTGGAAAGCTTAGCTGCAATATACAAACACCCAGGATCCCTTCTTGATTTGGTCTT	4080
Db	4021	GTTGAATTTGGAAAGCTTAGCTGCAATATACAAACACCCAGGATCCCTTCTTGATTTGGTCTT	4080
QY	4081	CCAAACAAATAGGCAATCACTGCTGTAAGAACCCAGGAAATGTCCTGAGTGAACGAATTTGG	4140
Db	4081	CCAAACAAATAGGCAATCACTGCTGTAAGAACCCAGGAAATGTCCTGAGTGAACGAATTTGG	4140
QY	4141	TTTCAGATGATGAAGAAGAGGAAGCGGCTTGGAAACAAATATATACAGAGAGCAACACA	4200
Db	4141	TTTCAGATGATGAAGAAGAGGAAGCGGCTTGGAAACAAATATATACAGAGAGCAACACA	4200
QY	4201	TGGAATTCAAACTTAGTGGAAGACAGCATCTGGGTGTGAGAGTGAACCAAGCGTCTCTGAG	4260
Db	4201	TGGAATTCAAACTTAGTGGAAGACAGCATCTGGGTGTGAGAGTGAACCAAGCGTCTCTGAG	4260
QY	4261	ACTGCTCAGGGCTATCTCTCACAAGTAGAATTTTAAACCACTCAGACAGAGGATATACATGCG	4320
Db	4261	ACTGCTCAGGGCTATCTCTCACAAGTAGAATTTTAAACCACTCAGACAGAGGATATACATGCG	4320
QY	4321	AACATTAACCTGATTAAGCTCCACAGAGAAATGGCTGAATACAGCTGTTTAGAACACGC	4380
Db	4321	AACATTAACCTGATTAAGCTCCACAGAGAAATGGCTGAATACAGCTGTTTAGAACACGC	4380
QY	4381	ATGGAGACCAAGCCTTCTTAACAGCTTACCTTCATCTAATAGTACACTCTTGCCCTTGAGG	4440
Db	4381	ATGGAGACCAAGCCTTCTTAACAGCTTACCTTCATCTAATAGTACACTCTTGCCCTTGAGG	4440
QY	4441	ACCTGCGAATCCAGAACCAAGCAGCATCAGAAAAGAGATTAATTACTTCAACAGAAAAGTA	4500
Db	4441	ACCTGCGAATCCAGAACCAAGCAGCATCAGAAAAGAGATTAATTACTTCAACAGAAAAGTA	4500
QY	4501	GTTGAATTCCTTATTAAGCAAGAAATCCAGAAAGGCTTTGCTGTCAGCAAGTTTAAAGTGTCTG	4560
Db	4501	GTTGAATTCCTTATTAAGCAAGAAATCCAGAAAGGCTTTGCTGTCAGCAAGTTTAAAGTGTCTG	4560
QY	4561	CAGATATCTTACACAGTAAATAATTAAGAACACAGAGATGGAAAAGGTCATCCCTCTCTAAT	4620



Db	4561	CNAGTAGTTCTACCAAGTAAAAAATAAGAACAGAGAGTGGAAAAAGTCTATCCCTTTAAAT	4620
Qy	4621	GCCCATCATTAGATAGATAGGTGTACATGCACAGTTCCTGGAGTCTTCAGAATAGA	4680
Db	4621	GCCCATCATTAGATAGATAGGTGTACATGCACAGTTCCTGGAGTCTTCAGAATAGA	4680
Qy	4661	ACTACCCATCTCAAGAGGAGACTATTAAAGTGTGTATGTGGAGAGCAACAGCTGGAA	4740
Db	4661	ACTACCCATCTCAAGAGGAGACTATTAAAGTGTGTATGTGGAGAGCAACAGCTGGAA	4740
Qy	4741	AGATGGGGCACACAGATTTCAGGAAACATCTTACTTGGCAAGCAAGATCTAGAGGAA	4800
Db	4741	AGTGTGGGCCACACAGATTTCAGGAAACATCTTACTTGGCAAGCAAGATCTAGAGGAA	4800
Qy	4801	CCCCCTTACCTGGAAATCTGGAAATACGCTCTTCTGTATGACCTTAATCTGATCCTTG	4860
Db	4801	CCCCCTTACCTGGAAATCTGGAAATACGCTCTTCTGTATGACCTTAATCTGATCCTTG	4860
Qy	4861	AAGACAGAGCCCCAGACTCAGCTCGATGGGCAATACCATCTTCAACCTGTGATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAAGCTCGATGGGCAATACCATCTTCAACCTGTGATTTGA	4920
Qy	4921	AAGTTCGCCAATTGAAAGTTCAGAAATCTGCCAGATCCAGCTCCTGCTATACTAGT	4980
Db	4921	AAGTTCGCCAATTGAAAGTTCAGAAATCTGCCAGATCCAGCTCCTGCTATACTAGT	4980
Qy	4961	ATACTGCTGGGTATAAATGCATGGAAAGTGTAGAGCGGAGAAAGCCAGAATTGACAG	5040
Db	4961	ATACTGCTGGGTATAAATGCATGGAAAGTGTAGAGCGGAGAAAGCCAGAATTGACAG	5040
Qy	5041	CTTCACAGAAAAGGCTCAACAAAAGATGTCATGGTGTGTCTGGCTGACCCAGAG	5100
Db	5041	CTTCACACGAAAAGGCTCAACAAAAGATGCCATGTTGTGTCTGGCTGACCCAGAG	5100
Qy	5101	AATTTATGCTGTGTACAGTTCGCCAGAAAACCAACATCATCTTTAACTAATTA	5160
Db	5101	AATTTATGCTGTGTACAGTTCGCCAGAAAACCAACATCATCTTTAACTAATTA	5160
Qy	5161	CTGAAAGAGACTCACTCATGTGTTATGAAAAAGATCTAGTGTGTGATGAAGGACAC	5220
Db	5161	CTGAAAGAGACTCACTCATGTGTTATGAAAAAGATCTAGTGTGTGATGAAGGACAC	5220
Qy	5221	TGAATATTTTCTAGCAATTCGGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTACCC	5280
Db	5221	TGAATATTTTCTAGCAATTCGGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTACCC	5280
Qy	5281	AGCTATTAATAAGAAAAGAAAAATCTCAATAGCAGATTTTAAATCAAGAGAGATGGG	5340
Db	5281	AGCTATTAATAAGAAAAGAAAAATCTCAATAGCAGATTTTAAATCAAGAGAGATGGG	5340
Qy	5341	TCATATGGAAGAACACCAAGAGTCCAAAGCGAGCAAGAAATCCAGAGACAGAAAGATCT	5400
Db	5341	TCATATGGAAGAACACCAAGAGTCCAAAGCGAGCAAGAAATCCAGAGACAGAAAGATCT	5400
Qy	5401	TCAGAGGGCTTAGAAATGTGTCTATGCGGCCCTTACCAACATGCCCCACAGATCAATCG	5460
Db	5401	TCAGAGGGCTTAGAAATGTGTCTATGCGGCCCTTACCAACATGCCCCACAGATCAATCG	5460
Qy	5461	AATGATAGTACAGCTGTGTGCTTCTGTGGTGAAGAGCTTTCATCATTCACCCCTTG	5520
Db	5461	AATGATAGTACAGCTGTGTGCTTCTGTGGTGAAGAGCTTTCATCATTCACCCCTTG	5520
Qy	5521	GCACAGGTCTCACCCCAATTTGTTGTCTCAGCCAGATCCCTGACAGAGAGCAATGGCT	5580
Db	5521	GCACAGGTCTCACCCCAATTTGTTGTCTCAGCCAGATCCCTGACAGAGAGCAATGGCT	5580
Qy	5581	TCGATGCAATTGGGCAAGATGTGTGAGGACGCTGTGTGACCCGAAAGAGGATTTGGACA	5640
Db	5581	TCGATGCAATTGGGCAAGATGTGTGAGGACGCTGTGTGACCCGAAAGAGGATTTGGACA	5640
Qy	5641	GTGTAGCACTCTACCACTGCGAGAGCTGGACACTTACTGATACCCAGATCCGCCACA	5700

DB	5641	GGTGACACTCTCACAGTCCAGAGCGTCGGACACTACTACTATATACCACCAAGATCCCCCACA	5700
OY	5701	GCCTACTGA 5711 	
DB	5701	GCCTACTGA 5711	
RESULT	5		
ID	V46458	standard; cDNA; 5711 BP.	
AC	V46458;		
DT	18-NOV-1998	(first entry)	
DE	Human BRCA1 omi2 polymorphism #1 cDNA.		
KM	polymorphism; susceptibility; anti-oncogene; tumour suppressor;		
KW	chromosome 17q; ss.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	120..5711	
FT		/tag= a	
FT	variation	/product= "BRCA1 omi2 protein"	
FT		2201	
FT		/tag= b	
FT		/note= "this polymorphic variation can be a C or T nucleotide"	
PN	US5750400-A.		
PD	12-MAY-1998		
PF	12-FEB-1997; 798691.		
PR	12-FEB-1996; US-598591.		
PA	12-FEB-1997; US-798691.		
PI	(ONCO-) ONCORMED INC.		
PI	Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,		
PI	Schelter DB, Zeng B:		
DR	WPI: 98-296774/26.		
PT	BRCA1 omi gene coding sequences - useful for distinguishing between		
PT	polymorphisms and mutation(s) in the screening for predisposing to		
PT	breast or ovarian cancer		
PS	Claim 2e: Page -: 54pp; English.		
CC	This sequence encodes a human BRCA1 (breast and ovarian cancer		
CC	predisposing gene) omi2 gene in which a polymorphic variation occurs at		
CC	nucleotide 2201. This sequence and other polymorphic variations of this		
CC	sequence are useful for the identification of an individual who may or		
CC	may not have an increased susceptibility to breast or ovarian cancer.		
CC	The sequences used identify gene changes which are due to polymorphisms,		
CC	rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour		
CC	suppressor) which is involved in genetic inheritance of cancers,		
CC	especially breast and ovarian cancer. It is found at human chromosome 17q		
CC	which is known to be linked to cancer susceptibility, especially breast		
CC	cancer. Cells containing a mutation in this gene lose the wild-type		
CC	function of BRCA1 and are more susceptible to cancers.		
CC	NOTE: This sequence does not appear in the specification but has been		
CC	created from the wild type BRCA1 omi2 gene represented in V46449.		
SEQ	Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1382 T;		
Query Match	100.0%; Score 5710.6; DB 1; Length 5711;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
OY	1	AGCGCGTGAGACTCCGGAACCCCGACACAGGCGTGGGGTTCTCGAATACTGGGCC 60	
DB	1	AAGTGGCTGAGACTTCTCGAGACCCCGACAGGCTGTGGGTTCTCGAATACTGGGCC 60	
OY	61	CCTGGCTCAGAGGCCCTTCAACCTCTGCTCTGGGTAAGTTCAATTGGACAGAAGAAA 120	
DB	61	CCTGGCTCAGAGGCCCTTCAACCTCTGCTCTGGGTAAGTTCAATTGGACAGAAGAAA 120	
OY	121	TGGATTATCTGCTCTTGGCGTTGAAGAAGTAAAGTATTAATCTATTCAGAGAAA 180	
DB	121	TGGATTATCTGCTCTTGGCGTTGAAGAAGTAAAGTATTAATCTATTCAGAGAAA 180	
OY	181	TCTTAGAGTGTCCCATCTGCTGTGAGTTGATCAAGAACTGTCTCCCAAGAGTGTAC 240	

D	b	181	TCCTAGAGCTGCCATCTGTCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTACC	240
Q	y	241	ACATATTTTGGAAATTTTGCATGCTGAAACCTTCACACGAGAAGAAAGGCGCTTCACAGT	300
D	b	241	ACATATTTTGGAAATTTTGCATGCTGAAACCTTCACACGAGAAGAAAGGCGCTTCACAGT	300
Q	y	301	GTCCTTTATGTAAAGATATATACCAAAAGAGCGCTACAGAAAGTACAGATTTAGTC	360
D	b	301	GTCCTTTATGTAAAGATATATATACCAAAAGAGCGCTACAGAAAGTACAGATTTAGTC	360
Q	y	361	AACCTGTGAAGAGCTATTTGAAGATCATTTGTGCTTTTCAGTTGACATGACAGGTTGGAGT	420
D	b	361	AACCTGTGAAGAGCTATTTGAAGATCATTTGTGCTTTTCAGTTGACATGACAGGTTGGAGT	420
Q	y	421	ATGCAAAACAGCTATTAATTTTGGCAAAAAGAAAATTAACCTCTCCTGACATCTTAAGATG	480
D	b	421	ATGCAAAACAGCTATTAATTTTGGCAAAAAGAAAATTAACCTCTCCTGACATCTTAAGATG	480
Q	y	481	AAGTTTCTATCATCCAAAGATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG	540
D	b	481	AAGTTTCTATCATCCAAAGATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG	540
Q	y	541	AACCCGAAATCTCTCTTGGCAGAAACAGTCTCAGTGTCCAGTCTCTAACCCTTGGA	600
D	b	541	AACCCGAAATCTCTCTTGGCAGAAACAGTCTCAGTGTCCAGTCTCTAACCCTTGGA	600
Q	y	601	CTGTGAGAACTCTGAGCAAAAGCAGCGGATACAACTCAAAAGAGTCTGTCTACATG	660
D	b	601	CTGTGAGAACTCTGAGCAAAAGCAGCGGATACAACTCAAAAGAGTCTGTCTACATG	660
Q	y	661	AATGGGATCTGATTTCTCTGAAAGTACCGTTAATTAAGCAACTTATGCACTGGGAG	720
D	b	661	AATGGGATCTGATTTCTCTGAAAGTACCGTTAATTAAGCAACTTATGCACTGGGAG	720
Q	y	721	ATCAGAATTTGTACAAATCAACCCCTCAAGGAACCGGATGAATCAGTTGGATTCTG	780
D	b	721	ATCAGAATTTGTACAAATCAACCCCTCAAGGAACCGGATGAATCAGTTGGATTCTG	780
Q	y	781	CAAAAAGGCTGCTTGATTTTCTGAGAGGATGTAACAAAATCTGMAATCATCAAC	840
D	b	781	CAAAAAGGCTGCTTGATTTTCTGAGAGGATGTAACAAAATCTGMAATCATCAAC	840
Q	y	841	CCAGTAAATTAATGATTTGACACCACTGAGAAAGCGTGCAGCTGAGAGCATCCAGAAAGT	900
D	b	841	CCAGTAAATTAATGATTTGACACCACTGAGAAAGCGTGCAGCTGAGAGCATCCAGAAAGT	900
Q	y	901	ATCAGGATAGTCTGTTCAAACTGATGTGAGAGCATGTGGCAAAATCTCATGCCA	960
D	b	901	ATCAGGATAGTCTGTTCAAACTGATGTGAGAGCATGTGGCAAAATCTCATGCCA	960
Q	y	961	GCTCATTACAGATGAGAACAGAGTTTATTACTACTAAAGACAGAAATGATGAGAA	1020
D	b	961	GCTCATTACAGATGAGAACAGAGTTTATTACTACTAAAGACAGAAATGATGAGAA	1020
Q	y	1021	AGGCTGAATTTCTGTAATTAAGCAAAAGCGCTGCTAGCAAGAGGCCAATATCAANT	1080
D	b	1021	AGGCTGAATTTCTGTAATTAAGCAAAAGCGCTGCTAGCAAGAGGCCAATATCAANT	1080
Q	y	1081	GGGCTGGAAGTAAGAAACATGTAATGATAGGCGAGTCCAGACAGAAAAAAGGTAG	1140
D	b	1081	GGGCTGGAAGTAAGAAACATGTAATGATAGGCGAGTCCAGACAGAAAAAAGGTAG	1140
Q	y	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGGAATTAAGCAGAACTGCCATCT	1200
D	b	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGGAATTAAGCAGAACTGCCATCT	1200
Q	y	1201	CAGGAATCTCTAGAGATTAAGTAATGTTCTTGGATTAACACTTAATAGCAGCATTCGA	1260
D	b	1201	CAGGAATCTCTAGAGATTAAGTAATGTTCTTGGATTAACACTTAATAGCAGCATTCGA	1260
Q	y	1261	AAGTTAATGAGTGGTTTCCAGAGTGAAGTGTAGTTAGTTCTGATACATCATGATG	1320
D	b	1261	AAGTTAATGAGTGGTTTCCAGAGTGAAGTGTAGTTAGTTCTGATACATCATGATG	1320

---

Q	y	1321	GGGAGCTGAATCAAAATGCCAAAGTAGCTGATTTAGAGCGTTCTTAATAGAGTAGATG	1380
D	b	1321	GGGAGCTGAATCAAAATGCCAAAGTAGCTGATTTAGAGCGTTCTTAATAGAGTAGATG	1380
Q	y	1381	AATATTCGTGTTCTTCAGAGAAAAATAGACTTACTGGCCATGATCCCTCATGAGCTTTAA	1440
D	b	1381	AATATTCGTGTTCTTCAGAGAAAAATAGACTTACTGGCCATGATCCCTCATGAGCTTTAA	1440
Q	y	1441	TATGTAAAGTGAAGAGTCTACATCCAAATCAGTAGAGTAATATTGAAGACAAAAATAT	1500
D	b	1441	TATGTAAAGTGAAGAGTCTACATCCAAATCAGTAGAGTAATATTGAAGACAAAAATAT	1500
Q	y	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCATGTAAGTAAATC	1560
D	b	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCCCTCCCAACTTAAGCATGTAAGTAAATC	1560
Q	y	1561	TAAATATGAGACATTTGTCTAGCCACAGATTAATACAGAGCGTCCCTCACAATAA	1620
D	b	1561	TAAATATGAGACATTTGTCTAGCCACAGATTAATACAGAGCGTCCCTCACAATAA	1620
Q	y	1621	AATTAAGCGTAAAGAGACCTACATCAGGCTTCATCCTGAGAGATTTATCAAGAAAG	1680
D	b	1621	AATTAAGCGTAAAGAGACCTACATCAGGCTTCATCCTGAGAGATTTATCAAGAAAG	1680
Q	y	1681	CAGATTTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAGGGAACCTAACCAAGGAGC	1740
D	b	1681	CAGATTTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAGGGAACCTAACCAAGGAGC	1740
Q	y	1741	AGAATGCTCAGTGTATTAATTTCTAATAGTGTCTATGAGATTAACAAAGAGTGATT	1800
D	b	1741	AGAATGCTCAGTGTATTAATTTCTAATAGTGTCTATGAGATTAACAAAGAGTGATT	1800
Q	y	1801	CTATTCAAGATGAGAAAAATCTTAACCAATAGATCAGCAAAAAAGATCTGCTTTCA	1860
D	b	1801	CTATTCAAGATGAGAAAAATCTTAACCAATAGATCAGCAAAAAAGATCTGCTTTCA	1860
Q	y	1861	AAACGAAAGCTGAACCTATTAAGCAGAGTATTAAGCAATATGAGAACTGAATTAATGTC	1920
D	b	1861	AAACGAAAGCTGAACCTATTAAGCAGAGTATTAAGCAATATGAGAACTGAATTAATGTC	1920
Q	y	1921	ACAATTAAGAAAGCACTTAAGAAATAGGCTGAGAGAGAGTCTTACCAAGCAATATTC	1980
D	b	1921	ACAATTAAGAAAGCACTTAAGAAATAGGCTGAGAGAGAGTCTTACCAAGCAATATTC	1980
Q	y	1981	ATGCGCTTGAACCTAGTGTAGTGAATCTTAAGCCACCTAATTTAGTGAATTCGAA	2040
D	b	1981	ATGCGCTTGAACCTAGTGTAGTGAATCTTAAGCCACCTAATTTAGTGAATTCGAA	2040
Q	y	2041	TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAAAGTCAACCAACCAATCCAGTCA	2100
D	b	2041	TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAAAGTCAACCAACCAATCCAGTCA	2100
Q	y	2101	GGCAGACAGAAACCTCAACTCATGGAAGTAAAGAACTGCACTGAGGCCAAGAA	2160
D	b	2101	GGCAGACAGAAACCTCAACTCATGGAAGTAAAGAACTGCACTGAGGCCAAGAA	2160
Q	y	2161	GTAACAAGCCAAATGAACAGACAAATTAAGACATGACAGCATTTTCCAGAGCTGA	2220
D	b	2161	GTAACAAGCCAAATGAACAGACAAATTAAGACATGACAGCATTTTCCAGAGCTGA	2220
Q	y	2221	AGTTAACAAATGACACCTGGTCTTTTACTAAGTTCCTCAATACAGTGAACCTTAAGAT	2280
D	b	2221	AGTTAACAAATGACACCTGGTCTTTTACTAAGTTCCTCAATACAGTGAACCTTAAGAT	2280
Q	y	2281	TTGTCAATCTTACGCTTCCAAAGAGAGAAAAAGAAAGAAACAGTTAAAGTGT	2340
D	b	2281	TTGTCAATCTTACGCTTCCAAAGAGAGAAAAAGAAAGAAACAGTTAAAGTGT	2340
Q	y	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAGAAAGGTTTGCAGAACTG	2400
D	b	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAGAAAGGTTTGCAGAACTG	2400



```

Db 4561 CAGATAGTCTACCAAGTAAATAAGAACAGAGAGTGGAAAGTCCATCCCTTTAAAT 4620
QY 4621 GCCCATGATTAGATGATAGTGTGTACATGACAGAGTGTGGAGTGTTCAGAAATAGAA 4680
    |||||||
Db 4621 GCCCATGATTAGATGATAGTGTGTACATGACAGAGTGTGGAGTGTTCAGAAATAGAA 4680
QY 4681 ACTACCATCTCAAGAGAGAGCTCATTAAGTGTGTGTGTGAGAGACAAAGCTGGAAAG 4740
    |||||||
Db 4681 ACTACCATCTCAAGAGAGAGCTCATTAAGTGTGTGTGTGAGAGACAAAGCTGGAAAG 4740
QY 4741 AGTGTGGGCCACAGATTTGACGGAAACATCTTACTTGCAGAGGAGAGTCCAGAGGAA 4800
    |||||||
Db 4741 AGTGTGGGCCACAGATTTGACGGAAACATCTTACTTGCAGAGGAGAGTCCAGAGGAA 4800
QY 4741 AGTGTGGGCCACAGATTTGACGGAAACATCTTACTTGCAGAGGAGAGTCCAGAGGAA 4800
    |||||||
QY 4801 CCCCTTACTGGAATCTGGAAATCAGACCTCTTCTGTGATGACCCCTGAATCTGATCTTCTG 4860
    |||||||
Db 4801 CCCCTTACTGGAATCTGGAAATCAGACCTCTTCTGTGATGACCCCTGAATCTGATCTTCTG 4860
QY 4861 AAGACAGAGCCCGAGAGTCTGTGTGGACATACATCTTCAACCTTGCACTTGA 4920
    |||||||
Db 4861 AAGACAGAGCCCGAGAGTCTGTGTGGACATACATCTTCAACCTTGCACTTGA 4920
QY 4921 AAGTTCCTCAATTAAGTTGACAGATCTGCCAGAGTCCAGAGTCTGTCTCATCTACTG 4980
    |||||||
Db 4921 AAGTTCCTCAATTAAGTTGACAGATCTGCCAGAGTCCAGAGTCTGTCTCATCTACTG 4980
QY 4981 ATACTGCTGGTATATATGCAATGGAAGAAAGTGTGAGAGGAGAGGAGAGGAGAGGAGAG 5040
    |||||||
Db 4981 ATACTGCTGGTATATATGCAATGGAAGAAAGTGTGAGAGGAGAGGAGAGGAGAGGAGAG 5040
QY 5041 CTTCACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5100
    |||||||
Db 5041 CTTCACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5100
QY 5101 AATTATGCTGTGTACAGAGTTTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5160
    |||||||
Db 5101 AATTATGCTGTGTACAGAGTTTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5160
QY 5161 CTGAGAGAGTCTACATGTTTATGAAACAGATGCTGAGTGTGTGTGTGAGAGGAGGAGGAGGAG 5220
    |||||||
Db 5161 CTGAGAGAGTCTACATGTTTATGAAACAGATGCTGAGTGTGTGTGTGAGAGGAGGAGGAGGAGGAG 5220
QY 5221 TGAATATTTTCTAGAGATTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5280
    |||||||
Db 5221 TGAATATTTTCTAGAGATTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5280
QY 5281 AGCTATTTAAAGAAAGAAATGCTGATGATGAGATGATTTTGAATGAGAGGAGGAGGAGGAGGAG 5340
    |||||||
Db 5281 AGCTATTTAAAGAAAGAAATGCTGATGATGAGATGATTTTGAATGAGAGGAGGAGGAGGAGGAG 5340
QY 5341 TCATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5400
    |||||||
Db 5341 TCATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5400
QY 5401 TCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5460
    |||||||
Db 5401 TCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5460
QY 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
    |||||||
Db 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
QY 5521 GCACAGGTGTCCACCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5580
    |||||||
Db 5521 GCACAGGTGTCCACCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5580
QY 5581 TCATGCAATTTGGGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5640
    |||||||
Db 5581 TCATGCAATTTGGGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5640
QY 5641 GTGTAGAGTCTTCACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5700
    |||||||
Db 5641 GTGTAGAGTCTTCACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5700

```

```

QY 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 6
V46459
ID V46459 standard; cDNA; 5711 BP.
AC V46459;
DT 18-NOV-1998 (first entry)
DE Human BRCA1 om12 polymorphism #2 cDNA.
KW BRCA1; om12; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW chromosome 17q; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 120..5711
FT FT /*tag= a
FT FT /product= "BRCA1 om12 protein"
FT FT variation 2430
FT FT /*tag= b
FT FT /note= "This polymorphic variation can be a T or C
        nucleotide"
PN US5750400-A.
PD 12-MAY-1998.
PE 12-FEB-1997; 798691.
PR 12-FEB-1996; US-598591.
PR 12-FEB-1997; US-798691.
PA (ONCO-) ONCOMED INC.
PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,
PI Schelter DB, Zeng B;
DR WPI: 98-296774/26.
PT BRCA1 om1 gene coding sequences - useful for distinguishing between
PT polymorphism and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
PS Claim 2e: Page -: 54pp; English.
CC This sequence encodes a human BRCA1 (breast and ovarian cancer
CC predisposing gene) om12 gene in which a polymorphic variation occurs at
CC nucleotide 2430. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome 17q
CC which is known to be linked to cancer susceptibility, especially breast
CC cancer. Cells containing a mutation in this gene lose the wild-type
CC function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 om12 gene represented in V46449.
SQ Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1382 T;

Query Match 100.0%; Score 5710.6; DB 1; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGTGACCCGACAGGCTGTGGGGTTTCAAGTAACTGGGCC 60
    |||||||
Db 1 AGCTGCTGAGACTTCTGTGACCCGACAGGCTGTGGGGTTTCAAGTAACTGGGCC 60
QY 61 CTTGCGCTCAGAGAGGCTTCAACCTCTGCTGTGGTAAAGTTGATGGAACAGAAAGAAA 120
    |||||||
Db 61 CTTGCGCTCAGAGAGGCTTCAACCTCTGCTGTGGTAAAGTTGATGGAACAGAAAGAAA 120
QY 121 TGAATTTATGCTCTCTGCGGTTGAGAGATACAAATGTCATTAATGCTATGCAAAAA 180
    |||||||
Db 121 TGAATTTATGCTCTCTGCGGTTGAGAGATACAAATGTCATTAATGCTATGCAAAAA 180
QY 121 TGAATTTATGCTCTCTGCGGTTGAGAGATACAAATGTCATTAATGCTATGCAAAAA 180
    |||||||
Db 121 TGAATTTATGCTCTCTGCGGTTGAGAGATACAAATGTCATTAATGCTATGCAAAAA 180
QY 181 TCTTAGAGTGTCCCATGTGTGTGAGTGTGATCAAGAGACCTGTCCCAAAAGTGTGACC 240
    |||||||
Db 181 TCTTAGAGTGTCCCATGTGTGTGAGTGTGATCAAGAGACCTGTGTCCCAAAAGTGTGACC 240

```

QY	1321	GGAGTCGATCAAAATGCCAAAGTAGCTATGTATATGAGCGTCTCTAAATGAGGTATGAT	1380
Db	1321	GGGAGTCGAATCAAAGGCCAAAGTAGCTGATGTATATGAGCGTCTCTAAATGAGGTATGAT	1380
QY	1381	AATATCTGGTCTTCAGAGAAAATAGCTACTTGGCCAGTGTACCTCATGAGCGCTTAA	1440
Db	1381	AATATCTGGTCTTCAGAGAAAATAGCTACTTGGCCAGTGTACCTCATGAGCGCTTAA	1440
QY	1441	TATGTAAAAGTGAAGAGTTCACCTCCAAATCACTAGAGATATATTTGAAGCAAAATAT	1500
Db	1441	TATGTAAAAGTGAAGAGTTCACCTCCAAATCACTAGAGATATATTTGAAGCAAAATAT	1500
QY	1501	TTGGAAAACTATCGAGAGAGCGAAAGCTCCCAACTTAAGCCATGTACTGAAATC	1560
Db	1501	TTGGAAAACTATCGAGAGAGCGAAAGCTCCCAACTTAAGCCATGTACTGAAATC	1560
QY	1561	TAAATATGAGCAATTTGTACTGAGCCACAGATATATACAGAGCGTCCCTCCACAAATA	1620
Db	1561	TAAATATGAGCAATTTGTACTGAGCCACAGATATATACAGAGCGTCCCTCCACAAATA	1620
QY	1621	AATTTAAAGCCTTAAAGAGAGACCTACATCAGAGCCTTATCCTGAGATTTTATCAAGAA	1680
Db	1621	AATTTAAAGCCTTAAAGAGAGACCTACATCAGAGCCTTATCCTGAGATTTTATCAAGAA	1680
QY	1681	CAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATTAATCAGGGACTATACCAAGGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATTAATCAGGGACTATACCAAGGAGC	1740
QY	1741	AGAAATGCGACGTATGAATATTTACTAATGTGTCATAGAAATTAACAAAAGGTGAT	1800
Db	1741	AGAAATGCGACGTATGAATATTTACTAATGTGTCATAGAAATTAACAAAAGGTGAT	1800
QY	1801	CTATTTCAAGAAATGAGAAAATCCTTAACCAATAGAAATCAGTCGAAAAGAAATCGCTTCA	1860
Db	1801	CTATTTCAAGAAATGAGAAAATCCTTAACCAATAGAAATCAGTCGAAAAGAAATCGCTTCA	1860
QY	1861	AAACGAAAGCTGAACCTATAGACGACGATTAAGCAATATGGAATCTGAATTAATATTC	1920
Db	1861	AAACGAAAGCTGAACCTATAGACGACGATTAAGCAATATGGAATCTGAATTAATATTC	1920
QY	1921	ACAATTCAAAAGCACTTAAAAAGAAATAGGTGAGAGAAAGTCTTACCAAGCATATTC	1980
Db	1921	ACAATTCAAAAGCACTTAAAAAGAAATAGGTGAGAGAAAGTCTTACCAAGCATATTC	1980
QY	1981	ATGGCCTTGAACCTAGTACGATAGAAATATAGCCACCTATTTGTACTGAAATGCAAA	2040
Db	1981	ATGGCCTTGAACCTAGTACGATAGAAATATAGCCACCTATTTGTACTGAAATGCAAA	2040
QY	2041	TTGATAGTGTCTTACGACGTTGAAGAGATAAGAAAAAAAGTACAAACCAATGCCAGTCA	2100
Db	2041	TTGATAGTGTCTTACGACGTTGAAGAGATAAGAAAAAAAGTACAAACCAATGCCAGTCA	2100
QY	2101	GGCACAGCAAAACCTTCACTCATGTGAAGGTAAABAACCTGCACTGGAGCCAGAAGA	2160
Db	2101	GGCACAGCAAAACCTTCACTCATGTGAAGGTAAABAACCTGCACTGGAGCCAGAAGA	2160
QY	2161	GTAACAAGCCCAAATGAGACACACAAGTAAAAAGACATGACAGCATACTTCCAGAGCTGA	2220
Db	2161	GTAACAAGCCCAAATGAGACACACAAGTAAAAAGACATGACAGCATACTTCCAGAGCTGA	2220
QY	2221	AGTTAACAAATGACACCTGTCTTTACTAAGGTTCAAATACCAAGTGAACCTTAAAGAT	2280
Db	2221	AGTTAACAAATGACACCTGTCTTTACTAAGGTTCAAATACCAAGTGAACCTTAAAGAT	2280
QY	2281	TTGTTCATCTTACGCTTCCAAAGAGAAAAAGAAAGAACTAGAAACAGTTAAAGT	2340
Db	2281	TTGTTCATCTTACGCTTCCAAAGAGAAAAAGAAAGAACTAGAAACAGTTAAAGT	2340
QY	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTAAAGTGAAGAAAGGTTTTCGCAACTG	2400
Db	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTAAAGTGAAGAAAGGTTTTCGCAACTG	2400
QY	2401	AAAGATCTGATAGACATGACGATATTTCAATTTGTGTACTGTACTGATTAATGACACTCAG	2460



```
|||||:|||||
Db 2401 AAGAGCTGTAGAGTAGAGATTTTCATGTGACTGTACTGATTAGGCACTAGG 2460
Oy 2461 AAGATATCTGTTACTGGAAGTTAGCACTTAGGGAAGCAAAACGAACCAATTAAT 2520
Db 2461 AAGATATCTGTTACTGGAAGTTAGCACTTAGGGAAGCAAAACGAACCAATTAAT 2520
Oy 2521 GTGTGAGTCAGTGTGACGACATTTTGAAAACCCCAAGGAGCTAATTCTGTTTCCAAG 2580
Db 2521 GTGTGAGTCAGTGTGACGACATTTTGAAAACCCCAAGGAGCTAATTCTGTTTCCAAG 2580
Oy 2581 ATAAATGAAGATGACACAGAGGCTTAAATATCATTTGGGACATGAAGTTAAACACAGTC 2640
Db 2581 ATAAATGAAGATGACACAGAGGCTTAAATATCATTTGGGACATGAAGTTAAACACAGTC 2640
Oy 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAACTGATGCTCAGTATTTTCAGAAATCAT 2700
Db 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAACTGATGCTCAGTATTTTCAGAAATCAT 2700
Oy 2701 TCAAGGTTTCAAAAGCCCGACGTCTTTGCTCTGTTTCAAAATCCAGGAAATGCAGAAAGG 2760
Db 2701 TCAAGGTTTCAAAAGCCCGACGTCTTTGCTCTGTTTCAAAATCCAGGAAATGCAGAAAGG 2760
Oy 2761 AATGTGCAACATTTCTGCGCCACTTGGGTCCTTAAAGAAACAAGTCCAAAGTCACTT 2820
Db 2761 AATGTGCAACATTTCTGCGCCACTTGGGTCCTTAAAGAAACAAGTCCAAAGTCACTT 2820
Oy 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGATAGCTAATATCAAGCCTGTAC 2880
Db 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGATAGCTAATATCAAGCCTGTAC 2880
Oy 2881 AGACAGTTAATATCACTGCAGGCTTTCCTGTGGTGTGTCGAAAGATAGCCAGTTGATA 2940
Db 2881 AGACAGTTAATATCACTGCAGGCTTTCCTGTGGTGTGTCGAAAGATAGCCAGTTGATA 2940
Oy 2941 ATGCCAAATGTATCAAGAGAGGCTAGGTTTGTCTATCATCTCAGTTAGAGGCA 3000
Db 2941 ATGCCAAATGTATCAAGAGAGGCTAGGTTTGTCTATCATCTCAGTTAGAGGCA 3000
Oy 3001 ACGAAACGTGACTCATTTACTCCAAATAAACATGAGACTTTTACAAAACCATATCGTATAC 3060
Db 3001 ACGAAACGTGACTCATTTACTCCAAATAAACATGAGACTTTTACAAAACCATATCGTATAC 3060
Oy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAATGTAAGAAAATCTCTGAGG 3120
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAATGTAAGAAAATCTCTGAGG 3120
Oy 3121 AAAACTTTGAGGAACATTCATGTCACTGAAAGAGAAATGGAAATGAGAACATTCGAA 3180
Db 3121 AAAACTTTGAGGAACATTCATGTCACTGAAAGAGAAATGGAAATGAGAACATTCGAA 3180
Oy 3181 GTACAGTGACCAATTAACCGCTAATTAACATTAGAGAAAATGTTTAAAGAGCCAGCT 3240
Db 3181 GTACAGTGACCAATTAACCGCTAATTAACATTAGAGAAAATGTTTAAAGAGCCAGCT 3240
Oy 3241 CAAGCAATATTAATGAAGTTCACAGTACTAATGAAGTGGGCTCCAGTATTAAGAAA 3300
Db 3241 CAAGCAATATTAATGAAGTTCACAGTACTAATGAAGTGGGCTCCAGTATTAAGAAA 3300
Oy 3301 TAGGTTCCAGTATGAAAAATTCAAGCAGAACTAGTGAAGAAACAGAGGCCAAAATTGA 3360
Db 3301 TAGGTTCCAGTATGAAAAATTCAAGCAGAACTAGTGAAGAAACAGAGGCCAAAATTGA 3360
Oy 3361 ATGCTATGCTTAGATTAGGGGTTTGGCAACTGAGGTCATTAACAAGATCTTCTCGTGA 3420
Db 3361 ATGCTATGCTTAGATTAGGGGTTTGGCAACTGAGGTCATTAACAAGATCTTCTCGTGA 3420
Oy 3421 GTAATGTGAAGATCCTGAATTAAGAAAACGAAGATATGAAGAGTGTTCAGACGTGTA 3480
Db 3421 GTAATGTGAAGATCCTGAATTAAGAAAACGAAGATATGAAGAGTGTTCAGACGTGTA 3480
Oy 3481 ATACGATTTCTCTCCATCTGATTTAGATTAACTTAACAGCTATGGGAAGTATGTC 3540
Db 3481 ATACGATTTCTCTCCATCTGATTTAGATTAACTTAACAGCTATGGGAAGTATGTC 3540

Db 3481 ATACGATTTCTCTCCATCTGATTTAGATTAACTTAACAGCTATGGGAAGTATGTC 3540
Oy 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTAATTAAG 3600
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTAATTAAG 3600
Oy 3601 AAGATACATGTTTGTCTGAAATGACATTAAAGAAAAGTTCTCTTTTAAAGCAACG 3660
Db 3601 AAGATACATGTTTGTCTGAAATGACATTAAAGAAAAGTTCTCTTTTAAAGCAACG 3660
Oy 3661 TCCAGAAAGAGAGCTTTACAGAGAGTCTAGGCCCTTTCACCATACATTTGGCTCAGG 3720
Db 3661 TCCAGAAAGAGAGCTTTACAGAGAGTCTAGGCCCTTTCACCATACATTTGGCTCAGG 3720
Oy 3721 GTTACCGAAGAGGAGGCAAGAAATTAGAGTCTCAGAAAGAACTTATCTAGTAGATG 3780
Db 3721 GTTACCGAAGAGGAGGCAAGAAATTAGAGTCTCAGAAAGAACTTATCTAGTAGATG 3780
Oy 3781 AAGAGCTTCCCTGCTTCAACACTGTTTATTTGGTAAAGTAAACAATATACCTTCTAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCAACACTGTTTATTTGGTAAAGTAAACAATATACCTTCTAGT 3840
Oy 3841 CTACTAGCATATGACACCGTTGCTACCGAGTGTCTGTAAAGACAGAGAGAAATTAAT 3900
Db 3841 CTACTAGCATATGACACCGTTGCTACCGAGTGTCTGTAAAGACAGAGAGAAATTAAT 3900
Oy 3901 TATCATTTGAAGATATACCTTAAATGAATGATGACATGACAGATATATTTGGCAAGCATCTC 3960
Db 3901 TATCATTTGAAGATATGCTTAAATGAATGATGACATGACAGATATATTTGGCAAGCATCTC 3960
Oy 3961 AGGAACATCACTTATGAGGAAACAAAATGTTCTGCTAGCTGTTTCTTCAACAGTGA 4020
Db 3961 AGGAACATCACTTATGAGGAAACAAAATGTTCTGCTAGCTGTTTCTTCAACAGTGA 4020
Oy 4021 GTGAATTTGAAGACTGTGACTGCAAAATACAAACCCAGAGATCTTCTTGAATGGTCTT 4080
Db 4021 GTGAATTTGAAGACTGTGACTGCAAAATACAAACCCAGAGATCTTCTTGAATGGTCTT 4080
Oy 4081 CCAAAACAATGAGGATCATGCTGAAAGCCAGAGAGTGGTCTGAGTGAACAAGAAATGG 4140
Db 4081 CCAAAACAATGAGGATCATGCTGAAAGCCAGAGAGTGGTCTGAGTGAACAAGAAATGG 4140
Oy 4141 TTTGAGATATTAAGAAAGAGAGAGAGGCTTGGAGAAATATATCAAGAAAGCA 4200
Db 4141 TTTGAGATATTAAGAAAGAGAGAGAGGCTTGGAGAAATATATCAAGAAAGCA 4200
Oy 4201 TGGATTCAAACTTAGGTGAAGAGCATCTGGGTGAGAGTGAAGAAAGAGCTCTCTGAAG 4260
Db 4201 TGGATTCAAACTTAGGTGAAGAGCATCTGGGTGAGAGTGAAGAAAGAGCTCTCTGAAG 4260
Oy 4261 ACTGCTCAGGGCTATCTCTCTGAGAGTGAATTTAAACACTCAGCAGAGAGATACATGC 4320
Db 4261 ACTGCTCAGGGCTATCTCTCTGAGAGTGAATTTAAACACTCAGCAGAGAGATACATGC 4320
Oy 4321 AACATTAACCTGATTAAGGCTCCAGCAGGAAATGCGTGAACCTGGAAGCTGTGTTAAACAGC 4380
Db 4321 AACATTAACCTGATTAAGGCTCCAGCAGGAAATGCGTGAACCTGGAAGCTGTGTTAAACAGC 4380
Oy 4381 ATGGAGCCAGGCTTCTTAACAGCTACCTTCATCATTAAGTGAAGCTCTCTGAGG 4440
Db 4381 ATGGAGCCAGGCTTCTTAACAGCTACCTTCATCATTAAGTGAAGCTCTCTGAGG 4440
Oy 4441 ACCCTCGAAATCCAGAAACAAAGCAGATCAGAAAAGCGATTAACCTCAGCAAGAAAGTA 4500
Db 4441 ACCCTCGAAATCCAGAAACAAAGCAGATCAGAAAAGCGATTAACCTCAGCAAGAAAGTA 4500
Oy 4501 GTGAATTAACCTTAAGCCAGAAATCCAGAAAGGCTTCTGCTGACAAAGTGTGAGTGTCTG 4560
Db 4501 GTGAATTAACCTTAAGCCAGAAATCCAGAAAGGCTTCTGCTGACAAAGTGTGAGTGTCTG 4560
Oy 4561 CAGATAGTTCTACAGTAAATAAGAAACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620
Db 4561 CAGATAGTTCTACAGTAAATAAGAAACAGAGAGTGAAGAGTCAATCCCTCTTAAT 4620
```





Oy	241	ACATATTTTGCAAATTTTGCATGCTGAAACTCTCCAACGAGAAAGGGCTTCACAGT	300
Db	241	ACATATTTTGCAAATTTTGCATGCTGAAACTCTCCAACGAGAAAGGGCTTCACAGT	300
Oy	301	GGCCTTATGTAAAGATGATATTAACCAAAAGGAGCCTACAAAGATGCGAGATTATGTC	360
Db	301	GGCCTTATGTAAAGATGATATTAACCAAAAGGAGCCTACAAAGATGCGAGATTATGTC	360
Oy	361	AACTTGTGAAGAGCTATTTGAAAATCATTTGTGCTTTACGCTTGACACAGTTTGGAGT	420
Db	361	AACTTGTGAAGAGCTATTTGAAAATCATTTGTGCTTTACGCTTGACACAGTTTGGAGT	420
Oy	421	ATGCAAAACAGCTTAAATTTTGCAAAAAAGGAAATAACTCTCTGACATCTAAAGATG	480
Db	421	ATGCAAAACAGCTTAAATTTTGCAAAAAAGGAAATAACTCTCTGACATCTAAAGATG	480
Oy	481	AAATTCTATCATCCAAAGATGGGCTACGAAACCGTGCCAAAAAGACTTCTACGAGATG	540
Db	481	AAATTCTATCATCCAAAGATGGGCTACGAAACCGTGCCAAAAAGACTTCTACGAGATG	540
Oy	541	AAACCGAAAAATCCTTCCTTGACAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGGAA	600
Db	541	AAACCGAAAAATCCTTCCTTGACAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGGAA	600
Oy	601	CTGTGGAAGACTCTGAGGACAAAGCAGGGGATACAACTCTCAAAAGACGTCTCTACATG	660
Db	601	CTGTGGAAGACTCTGAGGACAAAGCAGGGGATACAACTCTCAAAAGACGTCTCTACATG	660
Oy	661	AAATTGGATCTGATTTGCTTCTGAGATACCGTAAATAAGGCACCTATATGCAAGTGGGAG	720
Db	661	AAATTGGATCTGATTTGCTTCTGAGATACCGTAAATAAGGCACCTATATGCAAGTGGGAG	720
Oy	721	ATCAAGAAATTTGTTACAAATCACCCCTCAAGGAAACAGGAGATGAATCAGTTGGATTCTG	780
Db	721	ATCAAGAAATTTGTTACAAATCACCCCTCAAGGAAACAGGAGATGAATCAGTTGGATTCTG	780
Oy	781	CAAAAAAGGCTGCTTGTGGAATTTTCTGAGACGGATGTACAAATATCTGACATCATCAC	840
Db	781	CAAAAAAGGCTGCTTGTGGAATTTTCTGAGACGGATGTACAAATATCTGACATCATCAC	840
Oy	841	CCAGTAAATATGATTTTGAACACACACCTAGAGAGCTGACAGCTGAGAGGATCCAGAAAAGT	900
Db	841	CCAGTAAATATGATTTTGAACACACACCTAGAGAGCTGACAGCTGAGAGGATCCAGAAAAGT	900
Oy	901	ATCAGGGTAGTTCTGTTTCAAACTTGCCATGTGAGCCATGTGGCACAATATCTCATGCCA	960
Db	901	ATCAGGGTAGTTCTGTTTCAAACTTGCCATGTGAGCCATGTGGCACAATATCTCATGCCA	960
Oy	961	GCTCATATACAGCATGAGACACGACGATTTATTACTCAATAAAGACAGATGATGTAGAAA	1020
Db	961	GCTCATATACAGCATGAGACACGATTTATTACTCAATAAAGACAGATGATGTAGAAA	1020
Oy	1021	AGGCTGAATTCGTATATTAAGAACAACAGCGCTGGCTTAGCAAGAGAGCCAACTAACAGAT	1080
Db	1021	AGGCTGAATTCGTATATTAAGAACAACAGCGCTGGCTTAGCAAGAGAGCCAACTAACAGAT	1080
Oy	1081	GGGCTTGAAGTAAGAAACATGTATATGATAGGGCGACTCCAGCAGCAAGAAAAAAGGTAG	1140
Db	1081	GGGCTTGAAGTAAGAAACATGTATATGATAGGGCGACTCCAGCAGCAAGAAAAAAGGTAG	1140
Oy	1141	ATCTGAATCTGATCCCCCTGTGTGAGAGAAAAAGATGGAATAGCAGAACTGCCATGCT	1200
Db	1141	ATCTGAATCTGATCCCCCTGTGTGAGAGAAAAAGATGGAATAGCAGAACTGCCATGCT	1200
Oy	1201	CAGAGATCTAGAGATGACTGGAAGATGTTCTTGGAATAACATAAATAGCAGCAATTGAGA	1260
Db	1201	CAGAGATCTAGAGATGACTGGAAGATGTTCTTGGAATAACATAAATAGCAGCAATTGAGA	1260
Oy	1261	AAATTAAATAGTGGTTTTCAGAGATGATGAACGTTAGGTTCTGATGACCTACATGATG	1320
Db	1261	AAATTAAATAGTGGTTTTCAGAGATGATGAACGTTAGGTTCTGATGACCTACATGATG	1320
Oy	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATTGACGTTCTTAATGAGGTAGATG	1380

Db	1321	GGGAGCTCGAATCCAATGCCAAATGACTGATGTGATTGGACGTTCTCPAATGAGGTGAAG	1380
Qy	1381	AATATCTCGTCTCTCAGAGAAAATAGACTTACTAGGCCACAGTCCCATGAGGGCTTTAA	1440
Db	1381	AATATCTCGTCTCTCAGAGAAAATAGACTTACTAGGCCACAGTCCCATGAGGGCTTTAA	1440
Qy	1441	TATGTAAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGTAATATTGAGACAAAATAT	1500
Db	1441	TATGTAAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGTAATATTGAGACAAAATAT	1500
Qy	1501	TTGGGAAAACTATTCGGAGAAAGGCAAGCCTCCCAACTTAAGCCATGTATACGAAAATC	1560
Db	1501	TTGGGAAAACTATTCGGAGAAAGGCAAGCCTCCCAACTTAAGCCATGTATACGAAAATC	1560
Qy	1561	TAAATATAGAGCATTTTGTACTAGCCACAGATAATACAAAGAGCCTCCCTCACAAATA	1620
Db	1561	TAAATATAGAGCATTTTGTACTAGCCACAGATAATACAAAGAGCCTCCCTCACAAATA	1620
Qy	1621	AATTAAGCGTAAAAAGAGACCTACATCAGGCCCTCATCCTGAGATTTTATCAGAAG	1680
Db	1621	AATTAAGCGTAAAAAGAGACCTACATCAGGCCCTCATCCTGAGATTTTATCAGAAG	1680
Qy	1681	CAGATTTGGCGATTCAAAAGAGCTCCCTAATATGATTAATCGGGAACATAACCAAGGAGC	1740
Db	1681	CAGATTTGGCGATTCAAAAGAGCTCCCTAATATGATTAATCGGGAACATAACCAAGGAGC	1740
Qy	1741	AGAAATGTCACGATAGTAATTTACTAATAGTGGTCATGAGATTAACAAAAAGTGAT	1800
Db	1741	AGAAATGTCACGATAGTAATTTACTAATAGTGGTCATGAGATTAACAAAAAGTGAT	1800
Qy	1801	CTATTCAGAATGAGAAAAATCTTAACCAATAGAAATCCTCGAAAAAGATGCTCTTCA	1860
Db	1801	CTATTCAGAATGAGAAAAATCTTAACCAATAGAAATCCTCGAAAAAGATGCTCTTCA	1860
Qy	1861	AAACGAAGCTGAACCTTAAGCGACGATTAAGCAATATGGAACCTCGAATTAATATCC	1920
Db	1861	AAACGAAGCTGAACCTTAAGCGACGATTAAGCAATATGGAACCTCGAATTAATATCC	1920
Qy	1921	ACAATTCAAAAGCGACTTAAGAAAGAAATGAGGTGAGAGGAAGTTCTTACACAGCATATC	1980
Db	1921	ACAATTCAAAAGCGACTTAAGAAAGAAATGAGGTGAGAGGAAGTTCTTACACAGCATATC	1980
Qy	1981	ATGCGCTTGAACCTAGTAGTAGTAAGAAATCTAAGCCACCTAATTGTACTGATTTGAAA	2040
Db	1981	ATGCGCTTGAACCTAGTAGTAGTAAGAAATCTAAGCCACCTAATTGTACTGATTTGAAA	2040
Qy	2041	TTGATAGTGTCTTACGACGTGAAGAGATTAAGAAAAAGTACAAACAATATGCCAGTCA	2100
Db	2041	TTGATAGTGTCTTACGACGTGAAGAGATTAAGAAAAAGTACAAACAATATGCCAGTCA	2100
Qy	2101	GGCAGACGAAAGACCTCAACTCATCGGAAGCTTAAGACACTGCACTGAGGCCAAGAA	2160
Db	2101	GGCAGACGAAAGACCTCAACTCATCGGAAGCTTAAGACACTGCACTGAGGCCAAGAA	2160
Qy	2161	GTAACAAGCCAAATGAACAGACAGTAAAAAGACATGACAGCGATCTTCCAGAGCTGA	2220
Db	2161	GTAACAAGCCAAATGAACAGACAGTAAAAAGACATGACAGCGATCTTCCAGAGCTGA	2220
Qy	2221	AGTTAACAAATGCACTGCTGTTCTTTACTAAGTTCGAATATACAGTGAATTAAGAT	2280
Db	2221	AGTTAACAAATGCACTGCTGTTCTTTACTAAGTTCGAATATACAGTGAATTAAGAT	2280
Qy	2281	TTTGCAATCCGATGCTTCCAAAGGAAGAAAAAABAAGAAACGTAGAAAGTAAAGGT	2340
Db	2281	TTTGCAATCCGATGCTTCCAAAGGAAGAAAAAABAAGAAACGTAGAAAGTAAAGGT	2340
Qy	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTAAAGTGAAGAAAGGTTTGGCAAATCG	2400
Db	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTAAAGTGAAGAAAGGTTTGGCAAATCG	2400
Qy	2401	AAAGATCTGATGAGAGTAGCAGTATTTCAATTGTTACTGTTACTGATTAATGCACTACGG	2460

Db 2401 AAGATCTGAGAGAGTAGCAGTATTTCTATGGTACTGGTACTGATTATGAGCTAGG 2460  
Qy 2461 AAGATCTGCTTACTGGAAGTTAGCAGCTAGGGAAGGCAAAAAAGCAAAATTAAT 2520  
Db 2461 AAGATCTGCTTACTGGAAGTTAGCAGCTAGGGAAGGCAAAAAAGCAAAATTAAT 2520  
Qy 2521 GTGAGATCAGTGTGAGCAGCTTTAAAAACCAGGAGCTTAATCATGTTGTCCAAAG 2580  
Db 2521 GTGAGATCAGTGTGAGCAGCTTTAAAAACCAGGAGCTTAATCATGTTGTCCAAAG 2580  
Qy 2581 ATATATGAATATGACACAGAGGCTTTAATGATCCATTGGGACATGAAGTTAACCACAGTC 2640  
Db 2581 ATATATGAATATGACACAGAGGCTTTAATGATCCATTGGGACATGAAGTTAACCACAGTC 2640  
Qy 2641 GGGAAACAGCATGAAATGGAAGAAAGTGAATGCTGCTAGTATTGTCAGATACAT 2700  
Db 2641 GGGAAACAGCATGAAATGGAAGAAAGTGAATGCTGCTAGTATTGTCAGATACAT 2700  
Qy 2701 TCAGGTTTCAGAGGCGCAGTCTATTGCTGTTTCAATCCAGAAATGCGAGAGAG 2760  
Db 2701 TCAGGTTTCAGAGGCGCAGTCTATTGCTGTTTCAATCCAGAAATGCGAGAGAG 2760  
Qy 2761 AATGTGCAACATTCCTGCGCAGTCTGGGTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTCCTGCGCAGTCTGGGTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGGAAGAAATCAAGAAAGATGAGTCTAATATCAAGCCTTAC 2880  
Db 2821 TTGAATGTGAACAAAGGAAGAAATCAAGAAAGATGAGTCTAATATCAAGCCTTAC 2880  
Qy 2881 AGACAGTATATATCAGTCGAGGCTTCTGTTGGTGTGTCAGAAAGATTAAGCCAGTTATA 2940  
Db 2881 AGACAGTATATATCAGTCGAGGCTTCTGTTGGTGTGTCAGAAAGATTAAGCCAGTTATA 2940  
Qy 2941 ATGCAATATGATGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
Db 2941 ATGCAATATGATGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
Qy 3001 ACGAACTGAGACTTACTCTCAAAATTAACATGAGCTTTTACAAACCCTATGCTATAC 3060  
Db 3001 ACGAACTGAGACTTACTCTCAAAATTAACATGAGCTTTTACAAACCCTATGCTATAC 3060  
Qy 3061 CACCACTTTTCCCATCAAGTCAATTTGTAAACATTAATGTAAGAAATCTGCTAAGG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTAAACATTAATGTAAGAAATCTGCTAAGG 3120  
Qy 3121 AAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAACCTGCCA 3180  
Db 3121 AAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAACCTGCCA 3180  
Qy 3181 GTACAGTGAACACATTAATGCGGTAAATACATTAAGAAAAATGTTTTTAAAGAACCCAGCT 3240  
Db 3181 GTACAGTGAACACATTAATGCGGTAAATACATTAAGAAAAATGTTTTTAAAGAACCCAGCT 3240  
Qy 3241 CAAGCATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTATGAAGAAATTCAGACAGAACTAGGTAGAAACAGAGGCGCAAAATTTGA 3360  
Db 3301 TAGGTTCCAGTATGAAGAAATTCAGACAGAACTAGGTAGAAACAGAGGCGCAAAATTTGA 3360  
Qy 3361 ATGCTATGCTTAGATTAAGGGGTTTTGCAACCTGAGTCTATTAACAAAGTCTTCTGAAA 3420  
Db 3361 ATGCTATGCTTAGATTAAGGGGTTTTGCAACCTGAGTCTATTAACAAAGTCTTCTGAAA 3420  
Qy 3421 GTATTTTGAAGCATCTCGAATAATAAAAAGCAAGAAATTAAGAAAGTGTTCAGACTTTA 3480  
Db 3421 GTATTTTGAAGCATCTCGAATAATAAAAAGCAAGAAATTAAGAAAGTGTTCAGACTTTA 3480  
Qy 3481 ATACAGATTTCTCTCATATCTGATTTCAAGTAATTAAGAACAGCTATGGAAGTAGTGC 3540  
Db 3481 ATACAGATTTCTCTCATATCTGATTTCAAGTAATTAAGAACAGCTATGGAAGTAGTGC 3540

Qy 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTAATAAAG 3600  
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTAATAAAG 3600  
Qy 3601 AAGATCTAGTTTGTGGAATAATGACATTAAGAAAGTCTGCTGTTTACGAAAAAGCG 3660  
Db 3601 AAGATCTAGTTTGTGGAATAATGACATTAAGAAAGTCTGCTGTTTACGAAAAAGCG 3660  
Qy 3661 TCCAGAAAGAGAGCTTAGCAGAGTCTAGCCCTTACCCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAAAGAGAGCTTAGCAGAGTCTAGCCCTTACCCATACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGATCTCAGAGAGAACTTATCTAGTAGAGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGATCTCAGAGAGAACTTATCTAGTAGAGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTCCCAACTTGTATTGGTAAAGTAAACATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTCCCAACTTGTATTGGTAAAGTAAACATATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGATAGCAGCAGTGTGCTACGAGTGTCTGCTAAGAACACAGAGAGAAATTA 3900  
Db 3841 CTACTAGGATAGCAGCAGTGTGCTACGAGTGTCTGCTAAGAACACAGAGAGAAATTA 3900  
Qy 3901 TATCATTTGAAGAAATAGCTTAATGACTGCAATACAGTAACAGTAATTTGGCAAGGATCTC 3960  
Db 3901 TATCATTTGAAGAAATAGCTTAATGACTGCAATACAGTAACAGTAATTTGGCAAGGATCTC 3960  
Qy 3961 AGGAACATCACTTATGTAAGAAACAAATGTTCTGTAGTCTGTTTCTTACAGTGA 4020  
Db 3961 AGGAACATCACTTATGTAAGAAACAAATGTTCTGTAGTCTGTTTCTTACAGTGA 4020  
Qy 4021 GTGAATTTGAGAGCTTGACGCAATATCAAAACCCAGAGATCCTTCTGATTTGTTCTT 4080  
Db 4021 GTGAATTTGAGAGCTTGACGCAATATCAAAACCCAGAGATCCTTCTGATTTGTTCTT 4080  
Qy 4081 CCAAAACAAATGAGGCACTAGTCTGAAAAGCCAGGAGTTGGTCTGAGTGAACAGAAATGG 4140  
Db 4081 CCAAAACAAATGAGGCACTAGTCTGAAAAGCCAGGAGTTGGTCTGAGTGAACAGAAATGG 4140  
Qy 4141 TTTCAGATGATGAAGAAAGGAACGGGCTTGGAAAGAAATTAATCAAGAGAACCAAGCA 4200  
Db 4141 TTTCAGATGATGAAGAAAGGAACGGGCTTGGAAAGAAATTAATCAAGAGAACCAAGCA 4200  
Qy 4201 TGGATTCAACTTAGTGAAGAGCAGATCTGGGTGAGAGTGAACAAGGCTCTGTAAG 4260  
Db 4201 TGGATTCAACTTAGTGAAGAGCAGATCTGGGTGAGAGTGAACAAGGCTCTGTAAG 4260  
Qy 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Db 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Qy 4321 AACATTAACCTGATTAAGAGCTCCAGCAGAGAAATGCTGAACATGAAAGCTGTGTAACAGC 4380  
Db 4321 AACATTAACCTGATTAAGAGCTCCAGCAGAGAAATGCTGAACATGAAAGCTGTGTAACAGC 4380  
Qy 4381 ATGGAGAGCAGCCTCTTAACAGTACCCCTTCATCAATTAAGTACTCTGCGCCCTTGAGG 4440  
Db 4381 ATGGAGAGCAGCCTCTTAACAGTACCCCTTCATCAATTAAGTACTCTGCGCCCTTGAGG 4440  
Qy 4441 ACCTGGGAAATCCAGAACCAAGCAGATCAGAAAAAGCAGATTAATCAAGAAAAAGTA 4500  
Db 4441 ACCTGGGAAATCCAGAACCAAGCAGATCAGAAAAAGCAGATTAATCAAGAAAAAGTA 4500  
Qy 4501 GTGAATTAACCTTAATTAAGCCAGAAATCCAGAAAGGCTTCTGCTGCAAGTTGAGGTGCTG 4560  
Db 4501 GTGAATTAACCTTAATTAAGCCAGAAATCCAGAAAGGCTTCTGCTGCAAGTTGAGGTGCTG 4560  
Qy 4561 CAGATAGTTCTACAGTAATAAAATTAAGAAACAGAGAGTGAAGAAAGTATCCCTTCTTAAT 4620  
Db 4561 CAGATAGTTCTACAGTAATAAAATTAAGAAACAGAGAGTGAAGAAAGTATCCCTTCTTAAT 4620

```

OY 4621 GCCCATCATTTAGTATGATAGTGGTACATGCAAGTTCCTGCGGAGCTTTCAGATAGAA 4680
    |||||||
Db 4621 GCCCATCATTTAGTATGATAGTGGTACATGCAAGTTCCTGCGGAGCTTTCAGATAGAA 4680
OY 4681 ACTACCATCTCTCAAGAGAGAGAGCTATTAGGTTGTTGATGTGAGAGACCAACAGCTGGAG 4740
    |||||||
Db 4681 ACTACCATCTCTCAAGAGAGAGAGCTATTAGGTTGTTGATGTGAGAGACCAACAGCTGGAG 4740
OY 4741 AGTCTGGGCGACACGATTTTGACGGAAACATCTTACTTCCAAAGGCAAGATCTAGAGGAA 4800
    |||||||
Db 4741 AGTCTGGGCGACACGATTTTGACGGAAACATCTTACTTCCAAAGGCAAGATCTAGAGGAA 4800
OY 4801 CCCCTTACTCGAATCTGGAATCAGCCTCTTCTGTATGACCCCTGGAATCTGATCTCTCTG 4860
    |||||||
Db 4801 CCCCTTACTCGAATCTGGAATCAGCCTCTTCTGTATGACCCCTGGAATCTGATCTCTCTG 4860
OY 4861 AAGACAGAGCCCCAGAGATCGCTGCTGTTGGCAACATACCATCTTCAACCTCTGATTTGA 4920
    |||||||
Db 4861 AAGACAGAGCCCCAGAGATCGCTGCTGTTGGCAACATACCATCTTCAACCTCTGATTTGA 4920
OY 4921 AAGTTCCTCCAAATTTGAAAGTTGACAGATCTGCCAGAGTCCAGCTGCTCTCATACTAGT 4980
    |||||||
Db 4921 AAGTTCCTCCAAATTTGAAAGTTGACAGATCTGCCAGAGTCCAGCTGCTCTCATACTAGT 4980
OY 4981 ATACTCTGGGTATATGCAATGGAAAGATGTGAGCAGAGGAGAGAACCCAGAAATGACAG 5040
    |||||||
Db 4981 ATACTCTGGGTATATGCAATGGAAAGATGTGAGCAGAGGAGAGAACCCAGAAATGACAG 5040
OY 5041 CTTCACAGAGAGGCTCAACAAAGAAATGTCATGTGTGTGCTGAGCTGACCCAGAGAG 5100
    |||||||
Db 5041 CTTCACAGAGAGGCTCAACAAAGAAATGTCATGTGTGTGCTGAGCTGACCCAGAGAG 5100
OY 5101 AATTTATGCTCGTGTACAGATTTGCCAGAAACACCATCACTTAACTTAATTAATTA 5160
    |||||||
Db 5101 AATTTATGCTCGTGTACAGATTTGCCAGAAACACCATCACTTAACTTAATTAATTA 5160
OY 5161 CTGAAGAGAGCTACTCATGTGTATGAAACAGATGTGATGTTGTGTGAAAGGAGAC 5220
    |||||||
Db 5161 CTGAAGAGAGCTACTCATGTGTATGAAACAGATGTGATGTTGTGTGAAAGGAGAC 5220
OY 5221 TGAATATTTTCTAGAGATTTGCGGAGAGAAATGGGTAGTACTATTTTGTGGTGACC 5280
    |||||||
Db 5221 TGAATATTTTCTAGAGATTTGCGGAGAGAAATGGGTAGTACTATTTTGTGGTGACC 5280
OY 5281 AGTCTATTAAAGAAAGAAATCTGTAATGACATGATTTTGAAGTCAAGAGAGATGG 5340
    |||||||
Db 5281 AGTCTATTAAAGAAAGAAATCTGTAATGACATGATTTTGAAGTCAAGAGAGATGG 5340
OY 5341 TCAATGGAAGAAACCAAGGTCACAAAGGAGAGAGAAATCCAGAGAGAGAAAGATCT 5400
    |||||||
Db 5341 TCAATGGAAGAAACCAAGGTCACAAAGGAGAGAGAAATCCAGAGAGAGAAAGATCT 5400
OY 5401 TCAGGGGGGTAGAAATCTGTGCTATGAGGCCCTTCAACCAACATGCCACAGATCAATGG 5460
    |||||||
Db 5401 TCAGGGGGGTAGAAATCTGTGCTATGAGGCCCTTCAACCAACATGCCACAGATCAATGG 5460
OY 5461 AATGATGATGATACAGCTGTGTGTGCTTCTGTGTGAAAGAGCTTTTCACTTCACTTGA 5520
    |||||||
Db 5461 AATGATGATGATACAGCTGTGTGTGCTTCTGTGTGAAAGAGCTTTTCACTTCACTTGA 5520
OY 5521 GCACAGGTCTCACCAATTTGTTGTGTGAGCAGATGCTGTGAGAGAGAGAGAGAGAGTGGT 5580
    |||||||
Db 5521 GCACAGGTCTCACCAATTTGTTGTGTGAGCAGATGCTGTGAGAGAGAGAGAGAGTGGT 5580
OY 5581 TCCATGCAATTTGGGAGAGATGTGTGAGGACCTGTGTGAGAGAGAGAGAGAGAGTGGTGGACA 5640
    |||||||
Db 5581 TCCATGCAATTTGGGAGAGATGTGTGAGGACCTGTGTGAGAGAGAGAGAGAGTGGTGGACA 5640
OY 5641 GGTGAGCATCTTACAGAGTGCAGAGAGCTGAGACCTACCTGATATCCCAAGATCCCCACACA 5700
    |||||||
Db 5641 GGTGAGCATCTTACAGAGTGCAGAGAGCTGAGACCTACCTGATATCCCAAGATCCCCACACA 5700
OY 5701 GCCACTACTGA 5711

```

```

Db 5701 GCCACTACTGA 5711
RESULT 8
ID V46461 standard; cDNA: 5711 BP.
AC V46461;
DC 18-NOV-1998 (first entry)
DE Human BRCA1 om12 polymorphism #4 cDNA.
KM BRCA1; om12; human; breast and ovarian cancer predisposing gene;
KM polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KM chromosome 17q; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 120..5711
FT /tag= a
FT /product= "BRCA1 om12 protein"
FT variation 3332
FT /tag= b
FT /note= "This polymorphic variation can be an A or G
          nucleotide"
PN US5750400-A.
PD 12-MAY-1998.
PF 12-FEB-1997; 798691.
PR 12-FEB-1996; US-588591.
PR 12-FEB-1997; US-798691.
PA (ONCO-) ONCORMED INC.
PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,
PI Schelter DB, Zeng B;
PI WPI: 98-296774/26.
PT BRCA1 om1 gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
PS Claim 2e; Page -: 54pp; English.
CC This sequence encodes a human BRCA1 (breast and ovarian cancer
CC predisposing gene) om12 gene in which a polymorphic variation occurs at
CC nucleotide 3332. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome 17q
CC which is known to be linked to cancer susceptibility, especially breast
CC cancer. Cells containing a mutation in this gene lose the wild-type
CC function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 om12 gene represented in V46449.
SQ Sequence 5711 BP; 1955 A; 1098 C; 1274 G; 1383 T;

Query Match 100.0%; Score 5710.6; DB 1; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTGCTGAGACTTCTGACCCGACCAAGGCTGTGGGGTTTCTCAGATTAAGTGGGCC 60
    |||||||
Db 1 AGCTGCTGAGACTTCTGACCCGACCAAGGCTGTGGGGTTTCTCAGATTAAGTGGGCC 60
OY 61 CCGGCGCTCAGAGAGGCTTCCACCTCTGCTGTGGTAAAGTCAATGGAAAGAA 120
    |||||||
Db 61 CCGGCGCTCAGAGAGGCTTCCACCTCTGCTGTGGTAAAGTCAATGGAAAGAA 120
OY 121 TGGATTATCTCTCTTCCGCTTGAAGAGTACAAATGCTTAATGCTATGAGAAA 180
    |||||||
Db 121 TGGATTATCTCTCTTCCGCTTGAAGAGTACAAATGCTTAATGCTATGAGAAA 180
OY 181 TCTTGAAGTGTCCCATCTGTGTGAGGTGATCAAGAAAGCTGTCTCCAAAGTGTGACC 240
    |||||||
Db 181 TCTTGAAGTGTCCCATCTGTGTGAGGTGATCAAGAAAGCTGTCTCCAAAGTGTGACC 240
OY 241 ACATATTTTGCAGAAATTTTGCATGCTGAAACTTCTCAACCAAGAAAGGCGCTTACAGT 300

```

|||||  
Db 241 ACATATTTGCAATTTTGGCATGCTGAAACCTTCCACACACAAAGAAAGGGCTTCACAGT 300  
Qy 301 GTCCCTTATATGAAAGATGATATAACCAAAAGAGCCTACAAAGAAAGTACGAGATTTAGTC 360  
Db 301 GTCCCTTATATGAAAGATGATATAACCAAAAGAGCCTACAAAGAAAGTACGAGATTTAGTC 360  
Qy 361 AACTTGTGAAGAGACTATGAAATTCATTTGTGCTTTACAGTTGACACAGGTTTGGAGT 420  
Db 361 AACTTGTGAAGAGACTATGAAATTCATTTGTGCTTTACAGTTGACACAGGTTTGGAGT 420  
Qy 421 ATGCAACAGCTATATTTTGCAAAAAGAAAAATACCTCCCTGAACATCTAAAGATG 480  
Db 421 ATGCAACAGCTATATTTTGCAAAAAGAAAAATACCTCCCTGAACATCTAAAGATG 480  
Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAAGACTTCTACAGAGTG 540  
Qy 541 AACCAGAAATCCTTCTCTGCGAGAAACCAAGTCTCAAGTCTCAACCTCTTAACTTGGAA 600  
Db 541 AACCAGAAATCCTTCTCTGCGAGAAACCAAGTCTCAAGTCTCAACCTCTTAACTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTCAAAAGACGTCTGTACATG 660  
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTCAAAAGACGTCTGTACATG 660  
Qy 661 AATTGGATCTGATCTCTCTGAGATACCCCTTAATAAAGCACTTATTTGCACTGTGGAG 720  
Db 661 AATTGGATCTGATCTCTCTGAGATACCCCTTAATAAAGCACTTATTTGCACTGTGGAG 720  
Qy 721 ATCAAGATTTGTCAAAATCACCCCTCAAGSACCAAGGATGAAATCACTTTGATTTCTG 780  
Db 721 ATCAAGATTTGTCAAAATCACCCCTCAAGSACCAAGGATGAAATCACTTTGATTTCTG 780  
Qy 781 CAAAAAGGCTGCTTGTGAATTTCTGAGAGGATGTAAACAAATACGAAATCATCAAC 840  
Db 781 CAAAAAGGCTGCTTGTGAATTTCTGAGAGGATGTAAACAAATACGAAATCATCAAC 840  
Qy 841 CCAGTAAATATGATTTGAAACCACTGAGAGCGTGAGAGGATGAGGATCAGAAAAAGT 900  
Db 841 CCAGTAAATATGATTTGAAACCACTGAGAGCGTGAGAGGATGAGGATCAGAAAAAGT 900  
Qy 901 ATCAGGATGCTTCTGTTCAAACTTGCATGTGAGCCATGTGGCAAAATCTCATGCA 960  
Db 901 ATCAGGATGCTTCTGTTCAAACTTGCATGTGAGCCATGTGGCAAAATCTCATGCA 960  
Qy 961 GCTCATACAGCATGAGAGACGAGCTTATACACATAAGAGAGATGATGAGAA 1020  
Db 961 GCTCATACAGCATGAGAGACGAGCTTATACACATAAGAGAGATGATGAGAA 1020  
Qy 1021 AGGCTGAATCTGTAAATAAAGCAAAAGCCTGCTTACGAAAGAGCCAAATACAGAT 1080  
Db 1021 AGGCTGAATCTGTAAATAAAGCAAAAGCCTGCTTACGAAAGAGCCAAATACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGATATAGCGGACTCCAGACACGAAAAAAGGATG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGATATAGCGGACTCCAGACACGAAAAAAGGATG 1140  
Qy 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAAAGATGGAATACGAGAAATGSCATGCT 1200  
Db 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAAAGATGGAATACGAGAAATGSCATGCT 1200  
Qy 1201 CAGAGAAATCTAGAGATAGTAAAGATGTTCTTGATTAACCTAAATAGCAGCATTCGA 1260  
Db 1201 CAGAGAAATCTAGAGATAGTAAAGATGTTCTTGATTAACCTAAATAGCAGCATTCGA 1260  
Qy 1261 AAGTAAATGATGTTTCCAGAAAGTATGAACTGTAGGTTCTGATGACTCAATGATG 1320  
Db 1261 AAGTAAATGATGTTTCCAGAAAGTATGAACTGTAGGTTCTGATGACTCAATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATCCAAAGTAGTATGATGAGGCTTAAATAGGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATCCAAAGTAGTATGATGAGGCTTAAATAGGATG 1380  
|||||

Db 1321 GGGAGTCTGAATCAAAATCCAAAGTAGTATGATGAGGCTTAAATAGGATG 1380  
Qy 1381 AATATTTGCTTCTCAGAGAAATAGACTTACTGGCCAGTATCTCATGAGGCTTAA 1440  
Db 1381 AATATTTGCTTCTCAGAGAAATAGACTTACTGGCCAGTATCTCATGAGGCTTAA 1440  
Qy 1441 TATGTAAGGAAAGAGTTCACATCCAAATCAGTAGAGATTAATTTGAAGACAAATAT 1500  
Db 1441 TATGTAAGGAAAGAGTTCACATCCAAATCAGTAGAGATTAATTTGAAGACAAATAT 1500  
Qy 1501 TTGGGAAACCTATCGAGAGAGAGGCAAGCCTCCCACTTAAGCCATGTAACCTGAAATC 1560  
Db 1501 TTGGGAAACCTATCGAGAGAGAGGCAAGCCTCCCACTTAAGCCATGTAACCTGAAATC 1560  
Qy 1561 TAAATATAGAGCATTTTGTACTGAGCCACAGATTAATACAGAGAGTCCCTCAAAATA 1620  
Db 1561 TAAATATAGAGCATTTTGTACTGAGCCACAGATTAATACAGAGAGTCCCTCAAAATA 1620  
Qy 1621 AATTAAAGCGTAAAGAGAGACCTACATCAGGCTTCAATCCCTGAGAGATTTATCAAGAA 1680  
Db 1621 AATTAAAGCGTAAAGAGAGACCTACATCAGGCTTCAATCCCTGAGAGATTTATCAAGAA 1680  
Qy 1681 CAGATTTGGCAGTCAAAAGACCTCTGAAATGATTAATACAGGAACTAACCAACGAGC 1740  
Db 1681 CAGATTTGGCAGTCAAAAGACCTCTGAAATGATTAATACAGGAACTAACCAACGAGC 1740  
Qy 1741 AGAATGGTCAAGTATGATTAATTAATAGTGTGATGAGATTAACCAAGGATG 1800  
Db 1741 AGAATGGTCAAGTATGATTAATTAATAGTGTGATGAGATTAACCAAGGATG 1800  
Qy 1801 CTATTCGAATGAGAAAAATCTCTAACCCATAGAAATCACTCGAAAAAGAAATCTCTTCA 1860  
Db 1801 CTATTCGAATGAGAAAAATCTCTAACCCATAGAAATCACTCGAAAAAGAAATCTCTTCA 1860  
Qy 1861 AAAGAAAGCTGAAGCTATTAAGCAGAGTATTAAGCAATATGAACTGAAATTAATATCC 1920  
Db 1861 AAAGAAAGCTGAAGCTATTAAGCAGAGTATTAAGCAATATGAACTGAAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAAGCCTAAAAAGATAGGCTGAGAGGAAAGTCTTCAACGAGCATATTC 1980  
Db 1921 ACAATTCAAAAAGCCTAAAAAGATAGGCTGAGAGGAAAGTCTTCAACGAGCATATTC 1980  
Qy 1981 ATGCGCTTGAACCTATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
Db 1981 ATGCGCTTGAACCTATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
Qy 2041 TTGATAGTGTCTAGAGAGAGAGATTAAGAAAAAGATTAACCAATAGCCAGTCA 2100  
Db 2041 TTGATAGTGTCTAGAGAGAGAGATTAAGAAAAAGATTAACCAATAGCCAGTCA 2100  
Qy 2101 GGCACAGCAGAAACCTACACTCATGGAAGGTAAGAACTGCAACTGAGCCAAAGAGA 2160  
Db 2101 GGCACAGCAGAAACCTACACTCATGGAAGGTAAGAACTGCAACTGAGCCAAAGAGA 2160  
Qy 2161 GTAAACAAGCCAAATGAACAGACAGTAAAGACATGACAGGATCTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAAGCCAAATGAACAGACAGTAAAGACATGACAGGATCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAAATGACACCTGCTTCTTCTTACTAGTGTCAAAATACCAAGTAAAGAT 2280  
Db 2221 AGTTAAACAAATGACACCTGCTTCTTCTTACTAGTGTCAAAATACCAAGTAAAGAT 2280  
Qy 2281 TTGTCAATCTAGCCTTCCAAAGAGAAAAAGAGAAACCTAGAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTAGCCTTCCAAAGAGAAAAAGAGAAACCTAGAAACAGTTAAAGTGT 2340  
Qy 2341 CTAAATATGCTGAAGAGACCCAAAGATCTCATGTTAATGAGAAAGGTTTGGAACTG 2400  
Db 2341 CTAAATATGCTGAAGAGACCCAAAGATCTCATGTTAATGAGAAAGGTTTGGAACTG 2400  
Qy 2401 AAAGATCTGTAAGAGAGAGATTTTCAATGAGTCTGAGTACTGATTAAGGCACTAGG 2460  
Db 2401 AAAGATCTGTAAGAGAGAGATTTTCAATGAGTCTGAGTACTGATTAAGGCACTAGG 2460  
|||||



OY 2461 AAGATCTCGTACTAGGAGTTAGCACTTAGGGAAGCCAAAAACAGAACCAATAAT 2520  
|||||  
DB 2461 AAGATCTCGTACTAGGAGTTAGCACTTAGGGAAGCCAAAAACAGAACCAATAAT 2520  
OY 2521 GTGTGATCGTGTGGCGCAATTTGAAAAACCCCAAGGACTAATTCATGTTGTTCCAAAG 2580  
|||||  
DB 2521 GTGTGATCGTGTGGCGCAATTTGAAAAACCCCAAGGACTAATTCATGTTGTTCCAAAG 2580  
OY 2581 ATAAATGAATGACACAGAGAGCTTTAAGTATCCATTGGGACATGAATTAACACAGTC 2640  
|||||  
DB 2581 ATAAATGAATGACACAGAGAGCTTTAAGTATCCATTGGGACATGAATTAACACAGTC 2640  
OY 2641 GGGAAACACATAGAAATGAGAGAAAGTGAACTTGATGCTCAGTATTTGCGAATACAT 2700  
|||||  
DB 2641 GGGAAACACACATAGAAATGAGAGAAAGTGAACTTGATGCTCAGTATTTGCGAATACAT 2700  
OY 2701 TCAGGTTTCAAGCGCCGACATTTGCTGTGTTTCAAAATCCAGGAATGCGAAGAG 2760  
|||||  
DB 2701 TCAGGTTTCAAGCGCCGACATTTGCTGTGTTTCAAAATCCAGGAATGCGAAGAG 2760  
OY 2761 AATGTCAACATTTCTGCCCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
|||||  
DB 2761 AATGTCAACATTTCTGCCCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
OY 2821 TTGAATGTGAACAAAGGAAGAAATACAGGAAGAATGAGTCTAATATCAAGCCTGTAC 2880  
|||||  
DB 2821 TTGAATGTGAACAAAGGAAGAAATACAGGAAGAATGAGTCTAATATCAAGCCTGTAC 2880  
OY 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTGGTTGTCAGAAAGATAGCCAGTTGATA 2940  
|||||  
DB 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTGGTTGTCAGAAAGATAGCCAGTTGATA 2940  
OY 2941 ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCTCACTCAGTTCAAGGCA 3000  
|||||  
DB 2941 ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCTCACTCAGTTCAAGGCA 3000  
OY 3001 AGGAACCTGACATCTATCTCCCAATTAACATGAGCTTTTACAAACCCTATGTATAC 3060  
|||||  
DB 3001 AGGAACCTGACATCTATCTCCCAATTAACATGAGCTTTTACAAACCCTATGTATAC 3060  
OY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAATGTAGAAAAATCTGCTAGAG 3120  
|||||  
DB 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAATGTAGAAAAATCTGCTAGAG 3120  
OY 3121 AAAACTTTAGGAACAATTCATGTCACTGAAAGAGAAATGGGAATGAGAACATTTCCA 3180  
|||||  
DB 3121 AAAACTTTAGGAACAATTCATGTCACTGAAAGAGAAATGGGAATGAGAACATTTCCA 3180  
OY 3181 GTACAGTGAACAATTTAGCCGTAATTAACATTTAGAAAAATGTTTTTAAGAACCCAGCT 3240  
|||||  
DB 3181 GTACAGTGAACAATTTAGCCGTAATTAACATTTAGAAAAATGTTTTTAAGAACCCAGCT 3240  
OY 3241 CAAGCAATATTATGAAGTAGTTCAGTACTAATGAAAGTGGGCTCCAGTATTATGAAA 3300  
|||||  
DB 3241 CAAGCAATATTATGAAGTAGTTCAGTACTAATGAAAGTGGGCTCCAGTATTATGAAA 3300  
OY 3301 TAGGTTCCAGTATGAAGAACATTCAGACAGACTAGGTAGAAAACAGAGGCCCAAAATGTA 3360  
|||||  
DB 3301 TAGGTTCCAGTATGAAGAACATTCAGACAGACTAGGTAGAAAACAGAGGCCCAAAATGTA 3360  
OY 3361 ATGCTATGTTAGTATGAGGGTTTTGCAACCTTAGGCTATTAACAAAGTCTTCTGGA 3420  
|||||  
DB 3361 ATGCTATGTTAGTATGAGGGTTTTGCAACCTTAGGCTATTAACAAAGTCTTCTGGA 3420  
OY 3421 GTAATTTAGCATCTGTAATTAAGCAAGAAATATGAAGAAGTAGTTCAGACGTGTA 3480  
|||||  
DB 3421 GTAATTTAGCATCTGTAATTAAGCAAGAAATATGAAGAAGTAGTTCAGACGTGTA 3480  
OY 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAAGTAAAGTATGAGGAGGAGTATGAGT 3540  
|||||  
DB 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAAGTAAAGTATGAGGAGGAGTATGAGT 3540

OY 3541 ATGCATCTCAGGTTTGTGAGACACCTGATGACCTGTTAGATGATGTTGAATTAAG 3600  
|||||  
DB 3541 ATGCATCTCAGGTTTGTGAGACACCTGATGACCTGTTAGATGATGTTGAATTAAG 3600  
OY 3601 AAGTACTAGTTTTGCGAAAAATGACATTAAGGAAGTCTGCTGTTTTTACAAAAGCG 3660  
|||||  
DB 3601 AAGTACTAGTTTTGCGAAAAATGACATTAAGGAAGTCTGCTGTTTTTACAAAAGCG 3660  
OY 3661 TCCAGAAAGAGAGCTTAGCAGAGTCTAGCCCTTTCACCCATACACTTTGGCTCAG 3720  
|||||  
DB 3661 TCCAGAAAGAGAGCTTAGCAGAGTCTAGCCCTTTCACCCATACACTTTGGCTCAG 3720  
OY 3721 GTTACCAAGAGGGGCCAAGAAATTAGATCTCAAGAGAACTTATCTAGTGAAGT 3780  
|||||  
DB 3721 GTTACCAAGAGGGGCCAAGAAATTAGATCTCAAGAGAACTTATCTAGTGAAGT 3780  
OY 3781 AAGAGCTTCCCTGCTTCAACACTGTTGTTATTTGTTAAAGTAAACATATACCTTCAGT 3840  
|||||  
DB 3781 AAGAGCTTCCCTGCTTCAACACTGTTGTTATTTGTTAAAGTAAACATATACCTTCAGT 3840  
OY 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTAAAGACACAGAGAGAAATTAT 3900  
|||||  
DB 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTAAAGACACAGAGAGAAATTAT 3900  
OY 3901 TATCATTTGAAGAAATAGCTTAATGACTGCACTAACCGAGTAAATTTGGCAAGCATCTC 3960  
|||||  
DB 3901 TATCATTTGAAGAAATAGCTTAATGACTGCACTAACCGAGTAAATTTGGCAAGCATCTC 3960  
OY 3961 AGGAACATCACTTAGTGAAGAAACAAATGTTCTGCTAGCTGTTTCTTACAGTGA 4020  
|||||  
DB 3961 AGGAACATCACTTAGTGAAGAAACAAATGTTCTGCTAGCTGTTTCTTACAGTGA 4020  
OY 4021 GTGAATTTGAAGACTTACTGCAAAATACAAACACCAGATCTTCTGATTTGTTCTT 4080  
|||||  
DB 4021 GTGAATTTGAAGACTTACTGCAAAATACAAACACCAGATCTTCTGATTTGTTCTT 4080  
OY 4081 CCAACCAATGAGGCAATCAGTCTGAAAGCCAGGAGTGTGTTGAGTCAAGAAATGG 4140  
|||||  
DB 4081 CCAACCAATGAGGCAATCAGTCTGAAAGCCAGGAGTGTGTTGAGTCAAGAAATGG 4140  
OY 4141 TTTCAATGATGAAGAAAGAGAAAGGAGGCTTGAAGAAATATATCAAGAGCAACGA 4200  
|||||  
DB 4141 TTTCAATGATGAAGAAAGAGAAAGGAGGCTTGAAGAAATATATCAAGAGCAACGA 4200  
OY 4201 TGGATTTCAAACCTTAGTGAAGCAGATCTGGGTGTGAGAGTAAACCAAGCCTCTGAAG 4260  
|||||  
DB 4201 TGGATTTCAAACCTTAGTGAAGCAGATCTGGGTGTGAGAGTAAACCAAGCCTCTGAAG 4260  
OY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACCACTGAGAGAGGATACCATGC 4320  
|||||  
DB 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACCACTGAGAGAGGATACCATGC 4320  
OY 4321 AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACCTAGACCTGTTAGAACAGC 4380  
|||||  
DB 4321 AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACCTAGACCTGTTAGAACAGC 4380  
OY 4381 ATGGAGGACAGCCTTCTTAACAGCTACCTTCCATCATTAAGTACTCTTGCCTTGAAG 4440  
|||||  
DB 4381 ATGGAGGACAGCCTTCTTAACAGCTACCTTCCATCATTAAGTACTCTTGCCTTGAAG 4440  
OY 4441 ACCTGCGAAATCCAGAACAAAGCAGATCAAGAAAAGCAGTATTAACTTCAAGAAAAGTA 4500  
|||||  
DB 4441 ACCTGCGAAATCCAGAACAAAGCAGATCAAGAAAAGCAGTATTAACTTCAAGAAAAGTA 4500  
OY 4501 GTGAATACCTTTAAGCCGAATTCAGAGAGGCTTCTGCTGACAGCAAGTTAGAGTCTG 4560  
|||||  
DB 4501 GTGAATACCTTTAAGCCGAATTCAGAGAGGCTTCTGCTGACAGCAAGTTAGAGTCTG 4560  
OY 4561 CAGATAGTTCTACAGTAAATAAAGAACACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
|||||  
DB 4561 CAGATAGTTCTACAGTAAATAAAGAACACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
OY 4621 GCCCATCATTAAGATGATGAGTGTGCTACATGACAGTTGCTTGGGAGTCTTCAAGATAGAA 4680



Db	4621	GCACCATTAGATGATGAGTGGTACATGACAGTTCCTCTGGAGTCTCAGATTAAGA	4680
Qy	4691	ACTACCATCTCAAGAGAGCTCTATTAAAGTGTGTATGTGGAGGACAACGCTGGAG	4740
Db	4681	ACTACCATCTCAAGAGAGCTCTATTAAAGTGTGTATGTGGAGGACMAACGCTGGAG	4740
Qy	4741	AGATGGGACCAAGATTTACGAAACATCTTACTTGGCAAGCAAGATCTAAGGGAA	4800
Db	4741	AGTGTGGCCACAGATTTACGAAACATCTTACTTGGCAAGCAAGATCTAAGGGAA	4800
Qy	4801	CCCTTACTCTGGAATCTGGAATACGCTCTTCTCTGATGACCTCGAATCTGATCTCTG	4860
Db	4801	CCCTTACTCTGGAATCTGGAATACGCTCTTCTCTGATGACCTCGAATCTGATCTCTG	4860
Qy	4861	AAGACAGAGCCCAAGATCTGAGCTCGTGGGCAACTTACCATCTTCAACCTCTGATTTGA	4920
Db	4861	AAGACAGAGCCCAAGATCTGAGCTCGTGGGCAACTTACCATCTTCAACCTCTGATTTGA	4920
Qy	4921	AAAGTCCCAATTTGAAGATTGAGAAATCTGCCAGAGTCCAGCTCTGTCTACTACTAG	4980
Db	4921	AAAGTCCCAATTTGAAGATTGAGAAATCTGCCAGAGTCCAGCTCTGTCTACTACTAG	4980
Qy	4981	ATACTGCTGGGTATAATGCAATGGAAAGAAAGTGTAGCGAGGAGAAAGCCAGATTTGAAG	5040
Db	4981	ATACTGCTGGGTATAATGCAATGGAAAGAAAGTGTAGCGAGGAGAAAGCCAGATTTGAAG	5040
Qy	5041	CTTCAACAGAAAGGGTCAACAAAAGATGTCATCGGTGGTGTCTGAGCTGACCCCAAG	5100
Db	5041	CTTCAACAGAAAGGGTCAACAAAAGATGTCATCGGTGGTGTCTGAGCTGACCCCAAG	5100
Qy	5101	AATTTATGCTGTGTACAGATTTGCCAGAAAACCCATCATCTTAACTAACTTAATTA	5160
Db	5101	AATTTATGCTGTGTACAGATTTGCCAGAAAACCCATCATCTTAACTAACTTAATTA	5160
Qy	5161	CTGAAGAGCATCACTCATGTGTATGAAAGACAGATGCTGAGTTGTGTGAAGGACAC	5220
Db	5161	CTGAAGAGCATCACTCATGTGTATGAAAGACAGATGCTGAGTTGTGTGAAGGACAC	5220
Qy	5221	TGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTATGCTATTCGTGGTGACCC	5280
Db	5221	TGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTATGCTATTCGTGGTGACCC	5280
Qy	5281	AGCTATTATAAGAAAGAAATATGCTGAATGAGCATATTTTGAATGCAGAGACATGTGG	5340
Db	5281	AGCTATTATAAGAAAGAAATATGCTGAATGAGCATATTTTGAATGCAGAGAGATGTGG	5340
Qy	5341	TCAATGGAAGAAACACCAAGGTCCTCAACGAGCAAGAAATCCGAGGACAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACACCAAGGTCCTCAACGAGGCAAGAAATCCGAGGACAGAAAGATCT	5400
Qy	5401	TCAGAGGGGCTAGAAATCTGTTGCTATGAGGCCCTTCCACCAATGCCACAGATCAACTGG	5460
Db	5401	TCAGAGGGGCTAGAAATCTGTTGCTATGAGGCCCTTCCACCAATGCCACAGATCAACTGG	5460
Qy	5461	AATGATAGGTACAGCTGTGTGGTGTCTGTGTGTAAGAGAGTTTCATCATTCACCTCTG	5520
Db	5461	AATGATAGGTACAGCTGTGTGGTGTCTGTGTGTAAGAGAGCTTTTCATCATTCACCTCTG	5520
Qy	5521	GCACAGGTGTCCACCCCAATTTGGTGTGTGAGCCAGCATGCTGTGACAGAGGACATGCT	5580
Db	5521	GCACAGGTGTCCACCCCAATTTGGTGTGTGAGCCAGCATGCTGTGACAGAGGACATGCT	5580
Qy	5581	TCGATGGAATTTGGGAGAGATGTGTGAGGACACTGTGTGATGCCGAAGTGGGTGTGGACA	5640
Db	5581	TCGATGGAATTTGGGAGAGATGTGTGAGGACACTGTGTGATGCCGAAGTGGGTGTGGACA	5640
Qy	5641	GTTAGACACTCTACAGTGTCCAGAGACTGTGACACTCACTGATATACCCAGATCCCCACA	5700
Db	5641	GTTAGACACTCTACAGTGTCCAGAGACTGTGACACTCACTGATATACCCAGATCCCCACA	5700
Qy	5701	GCACACTACTGA 5711	

RESULT	9
ID	V46462
AC	V46462 standard; cDNA; 5711 BP.
DE	18-NOV-1998 (first entry)
DEF	Human BRCA1 cml2 polymorphism #5 cDNA.
KW	BRCA1; cml2; human; breast and ovarian cancer predisposing gene;
KW	polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW	chromosome 17q; ss.
OS	Homo sapiens.
FT	Key
FT	Location/Qualifiers
FT	120..5711
FT	/tag- a
FT	/product= "BRCA1 cml2 protein"
FT	3667
FT	/tag- b
FT	/note= "this polymorphic variation can be an A or G nucleotide"
variation	
US5750400-A.	
12-MAY-1998.	
12-FEB-1997.	798691.
12-FEB-1996.	US-598591.
12-FEB-1997.	US-798691.
(ONCO- ) ONCORMED INC.	
Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,	
Scheller DB, Zeng B;	
WPI: 98-296774/26.	
BRCA1 cml2 gene coding sequences - useful for distinguishing between	
pt polymorphisms and mutation(s) in the screening for disposition to	
breast or ovarian cancer	
Claim 2e; Page : 54pp; English.	
This sequence encodes a human BRCA1 (breast and ovarian cancer	
predisposing gene) cml2 gene in which a polymorphic variation occurs at	
nucleotide 3667. This sequence and other polymorphic variations of this	
sequence are useful for the identification of an individual who may or	
may not have an increased susceptibility to breast or ovarian cancer.	
The sequences used identify gene changes which are due to polymorphisms,	
rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour	
suppressor) which is involved in genetic inheritance of cancers,	
especially breast and ovarian cancer. It is found at human chromosome 17q	
which is known to be linked to cancer susceptibility, especially breast	
cancer. Cells containing a mutation in this gene lose the wild-type	
function of BRCA1 and are more susceptible to cancers.	
CC NOTE: This sequence does not appear in the specification but has been	
created from the wild type BRCA1 cml2 gene represented in V46449.	
CC	
CC	
CC	
Sequence 5711 BP; 1955 A; 1098 C; 1274 G; 1383 T;	
Query Match	100.0%; Score 5710.6; DB 1; Length 5711;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AGCGCGCGAGACCTCCGAGACCCGACACGAGCGCTGGGTTCTCGATACGCGGC 60
DB	1 AGCTGCGTGAAGCTTCGAGACCCGACACGAGCGCTGGGTTCTCGATACGCGGC 60
QY	61 CCGCGCGTCAAGAGCGCTCAACCCCTCTGCTGGGTAAGTTCATGGAACGAAGAAA 120
DB	61 CCGCGCGTCAAGAGCGCTCAACCCCTCTGCTGGGTAAGTTCATGGAACGAAGAAA 120
QY	121 TGGATTATCTGCTCTTGGCGGTGAAGAAGTCAAAATGCTATTAAGTATGCGAANA 180
DB	121 TGGATTATCTGCTCTTGGCGGTGAAGAAGTCAAAATGCTATTAAGTATGCGAANA 180
QY	181 TCTTAGAGTATGCCATCTGCTGAGGATGATCAAGAACTGTCTCCCAAGATGTGACC 240
DB	181 TCTTAGAGTATGCCATCTGCTGAGGATGATCAAGAACTGTCTCCCAAGATGTGACC 240
QY	241 ACATATTTTGGAAATTTTGCATGCTGAACCTTCTCAACAGAAAGAAAGGCGCTTACAGT 300

Db 241 ACATATTTTGCATTTGCTGCTGAACTTTCACACAGAGAGAGAGGCGCTTACAGT 300  
QY 301 GTGCTTTATGTAAGATGATATACCAAAAGAGAGCTACAGAAAGTACGAGATTTAGTC 360  
Db 301 GTGCTTTATGTAAGATGATATACCAAAAGAGAGCTACAGAAAGTACGAGATTTAGTC 360  
QY 361 AACTTGTGAAGAGCTATTGAAATCATTTTGTCTTTACGCTTGACAGAGTTGGAGT 420  
Db 361 AACTTGTGAAGAGCTATTGAAATCATTTTGTCTTTACGCTTGACAGAGTTGGAGT 420  
QY 421 ATGCAAAACAGCTATATTTTGCACAAAAGAAATTAAGTCTGTAACATGTAAAGATG 480  
Db 421 ATGCAAAACAGCTATATTTTGCACAAAAGAAATTAAGTCTGTAACATGTAAAGATG 480  
QY 481 AACTTCTATCATCAAAAGATGGGCTACAGAAACCGTCCCAAAAGATTCTACAGAGTG 540  
Db 481 AACTTCTATCATCAAAAGATGGGCTACAGAAACCGTCCCAAAAGATTCTACAGAGTG 540  
QY 541 AACCCGAAAATCCTCTCTGTCAGAGAAACAGTCTCATGTCTCAACTCTTAACCTTGGAA 600  
Db 541 AACCCGAAAATCCTCTCTGTCAGAGAAACAGTCTCATGTCTCAACTCTTAACCTTGGAA 600  
QY 601 CTGTGAGAACTGTAGAGACAAAGCAGGAGATACAACTCAAAAGAGCGTGTCTACATTTG 660  
Db 601 CTGTGAGAACTGTAGAGACAAAGCAGGAGATACAACTCAAAAGAGCGTGTCTACATTTG 660  
QY 661 AATTGGATCTGATTTCTTCTGAGAGATACCGTTAATAAGGCACTTATTGCAGTGGGAG 720  
Db 661 AATTGGATCTGATTTCTTCTGAGAGATACCGTTAATAAGGCACTTATTGCAGTGGGAG 720  
QY 721 ATCAAGAAATGTTACAAATACCCCTCAAGGAAACAGGAGTGAATGATTTGATTTCTG 780  
Db 721 ATCAAGAAATGTTACAAATACCCCTCAAGGAAACAGGAGTGAATGATTTGATTTCTG 780  
QY 781 CAAAAAAGGCTGCTTGTGATTTTCTGAGAGAGATGTACAAATATCTGAACATGATCAAC 840  
Db 781 CAAAAAAGGCTGCTTGTGATTTTCTGAGAGAGATGTACAAATATCTGAACATGATCAAC 840  
QY 841 CCAATTAATTAATGATTTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGCAATCCAGAAAAT 900  
Db 841 CCAATTAATTAATGATTTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGCAATCCAGAAAAT 900  
QY 901 ATCAGAGTGTGTTGTTTCAACTGTGAGAGGCAATGTGAGCAAAATCTGATGCA 960  
Db 901 ATCAGAGTGTGTTGTTTCAACTGTGAGAGGCAATGTGAGCAAAATCTGATGCA 960  
QY 961 GCTCATTAAGCATGAGAACAGCAGTTATTACTACTAAAGACAGATGATGTAGAAA 1020  
Db 961 GCTCATTAAGCATGAGAACAGCAGTTATTACTACTAAAGACAGATGATGTAGAAA 1020  
QY 1021 AAGCTTAATTTCTGTAATTAAGCAACAGCCTGGCTTTAGCAAGAGGCCAATTAACAGAT 1080  
Db 1021 AAGCTTAATTTCTGTAATTAAGCAACAGCCTGGCTTTAGCAAGAGGCCAATTAACAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATATAGGGGAGTCCCGAGACAGAGAAAAGGATG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATATAGGGGAGTCCCGAGACAGAGAAAAGGATG 1140  
QY 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGAATAGCAGAAAATGCGCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGAATAGCAGAAAATGCGCATGCT 1200  
QY 1201 CAGAGAACTCTAGAGATGAGTGAAGATGTTCTTGATTAACACTAAATAGCAGCTTTCAGA 1260  
Db 1201 CAGAGAACTCTAGAGATGAGTGAAGATGTTCTTGATTAACACTAAATAGCAGCTTTCAGA 1260  
QY 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATGAATGATGTTGAGTGTGATGATGATGATG 1320  
Db 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATGAATGATGTTGAGTGTGATGATGATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTGATGATGAGAGTCTTAATGAGTATGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTGATGATGAGAGTCTTAATGAGTATGATG 1380

---

QY 1381 AATATCTGTTCTTGAGAGAAAATAGACTTACTGCGCAGTATCTCATGAGGCTTTAA 1440  
Db 1381 AATATCTGTTCTTGAGAGAAAATAGACTTACTGCGCAGTATCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTCTACTCCAAATCACTAAGAGATATATTGAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTCTACTCCAAATCACTAAGAGATATATTGAAGCAAAATAT 1500  
QY 1501 TTGGGAAACCTATCGGAGAAAGGCAAGCCCTCCCACTTAAGCCATGTAAGTGAATATC 1560  
Db 1501 TTGGGAAACCTATCGGAGAAAGGCAAGCCCTCCCACTTAAGCCATGTAAGTGAATATC 1560  
QY 1561 TAATTAATGAGCATTTTGTACTGAGCCACAGATTAATACAGAGGCTCCCTCACAAATA 1620  
Db 1561 TAATTAATGAGCATTTTGTACTGAGCCACAGATTAATACAGAGGCTCCCTCACAAATA 1620  
QY 1621 AATTAAAGCGTAAAGAGAGCCATCAATCAAGCCCTGATCTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCGTAAAGAGAGCCATCAATCAAGCCCTGATCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGCGAGTTCAAAAGACTCTGAAATGATTAATCAGGAACTAACAACGAGAGC 1740  
Db 1681 CAGATTTGCGAGTTCAAAAGACTCTGAAATGATTAATCAGGAACTAACAACGAGAGC 1740  
QY 1741 AGAATGCTCAAGTGAATATTACTAATAGTGTGATGAGATTAACAAAGAGTGAAT 1800  
Db 1741 AGAATGCTCAAGTGAATATTACTAATAGTGTGATGAGATTAACAAAGAGTGAAT 1800  
QY 1801 CTATTCGATGAGAAAGAAATCCCAACCAATGAATCACTCGGAAAGAAATGCTTTCA 1860  
Db 1801 CTATTCGATGAGAAAGAAATCCCAACCAATGAATCACTCGGAAAGAAATGCTTTCA 1860  
QY 1861 AAAAGAAAGCTGAACCTATTAAGCAGCAGTATAAGCAATATGCACTGATTAATATTC 1920  
Db 1861 AAAAGAAAGCTGAACCTATTAAGCAGCAGTATAAGCAATATGCACTGATTAATATTC 1920  
QY 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGAGAGATCTTCAACAGCAGTATTC 1980  
Db 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGAGAGATCTTCAACAGCAGTATTC 1980  
QY 1981 ATGCGCTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
Db 1981 ATGCGCTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
QY 2041 TTGATAGTGTCTTACAGTGAAGATTAAGAAAAAGTAAACCAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTGTCTTACAGTGAAGATTAAGAAAAAGTAAACCAACCAATGCCAGTCA 2100  
QY 2101 GGCACAGCAGAAAACCTACAACTCATGAGAAAGTAAAGAACTGAGGCAAGAAAGA 2160  
Db 2101 GGCACAGCAGAAAACCTACAACTCATGAGAAAGTAAAGAACTGAGGCAAGAAAGA 2160  
QY 2161 GTPAACAGCAAAATGAACAGACAAATGAAGAAAGATGACAGGATCTTCCAGAGCTGA 2220  
Db 2161 GTPAACAGCAAAATGAACAGACAAATGAAGAAAGATGACAGGATCTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAAATGACCTGTTCTTACTAAGTGTCAATACAGTGAATTAAGAT 2280  
Db 2221 AGTTAAACAAATGACCTGTTCTTACTAAGTGTCAATACAGTGAATTAAGAT 2280  
QY 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAAAGTAAAGTGT 2340  
Db 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAAAGTAAAGTGT 2340  
QY 2341 CTATTAATGCTGAAGAGCCCAAGATCTCATGTTAAGTGAAGAGGTTTTCAGAAATG 2400  
Db 2341 CTATTAATGCTGAAGAGCCCAAGATCTCATGTTAAGTGAAGAGGTTTTCAGAAATG 2400  
QY 2401 AAGATCTGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460  
Db 2401 AAGATCTGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460

2461 AAATATCTGTTAGTGAAGTTAGCACTCTAGGGAAGGCAAAAAGAACCAATAAT 2520  
2461 AAATATCTGTTAGTGAAGTTAGCACTCTAGGGAAGGCAAAAAGAACCAATAAT 2520  
2521 GTGTGAGTCAAGTGTGAGCACTTTGAAAAACCCCAAGGACTAATTCATGTTGTTCGAAG 2580  
2521 GTGTGAGTCAAGTGTGAGCACTTTGAAAAACCCCAAGGACTAATTCATGTTGTTCGAAG 2580  
2581 ATATATGAATGACACAGAAAGCTTTAAGTATCCATTGGCAGATGAAGTTAACCAAGTC 2640  
2581 ATATATGAATGACACAGAAAGCTTTAAGTATCCATTGGCAGATGAAGTTAACCAAGTC 2640  
2641 GGGAAACAGCATGGAATGGAAGAAAGTGAATGCTGATGCTATTTGGAGAAATCAT 2700  
2641 GGGAAACAGCATGGAATGGAAGAAAGTGAATGCTGATGCTATTTGGAGAAATCAT 2700  
2701 TCAAGGTTTCAAGGCGCAGTCACTTGTCTGTTTCAAAATCCAGAAATGCAAGAGG 2760  
2701 TCAAGGTTTCAAGGCGCAGTCACTTGTCTGTTTCAAAATCCAGAAATGCAAGAGG 2760  
2761 AATGTGCAACATCTCTGCCACCTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
2761 AATGTGCAACATCTCTGCCACCTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
2821 TTGATATGGAACAAAGGAAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC 2880  
2821 TTGATATGGAACAAAGGAAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC 2880  
2881 AGACAGTAAATATATCATGCAAGGCTTCTGCTGTTGTCAGAAAGATAGCACTGTATA 2940  
2881 AGACAGTAAATATATCATGCAAGGCTTCTGCTGTTGTCAGAAAGATAGCACTGTATA 2940  
2881 AGACAGTAAATATATCATGCAAGGCTTCTGCTGTTGTCAGAAAGATAGCACTGTATA 2940  
2941 ATGCCAAATGATGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
2941 ATGCCAAATGATGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
3001 ACGAAATGAGCACTATACCTCAATTAACATGAGACTTTTACAAAACCCATATGCTATAC 3060  
3001 ACGAAATGAGCACTATACCTCAATTAACATGAGACTTTTACAAAACCCATATGCTATAC 3060  
3061 CACCACTTTTCCCATCAAGTCACTTGTGTTAAACTAATGTAAGAAATCTGTAGAGG 3120  
3061 CACCACTTTTCCCATCAAGTCACTTGTGTTAAACTAATGTAAGAAATCTGTAGAGG 3120  
3061 CACCACTTTTCCCATCAAGTCACTTGTGTTAAACTAATGTAAGAAATCTGTAGAGG 3120  
3121 AAAAATTGAGGAACATTCATGTCACCTGAAAGAGAAATGGAATGAGAACTTCCAA 3180  
3121 AAAAATTGAGGAACATTCATGTCACCTGAAAGAGAAATGGAATGAGAACTTCCAA 3180  
3181 GTACAGTACACATTAAGCCGTAAATTAACATTAAGAAATGTTTAAAGAACCCAGCT 3240  
3181 GTACAGTACACATTAAGCCGTAAATTAACATTAAGAAATGTTTAAAGAACCCAGCT 3240  
3181 GTACAGTACACATTAAGCCGTAAATTAACATTAAGAAATGTTTAAAGAACCCAGCT 3240  
3241 CAAGCAATTAATTAAGAGTGTCCAGTACTAATGAAGTGGCTCCAGTATTAATGA 3300  
3241 CAAGCAATTAATTAAGAGTGTCCAGTACTAATGAAGTGGCTCCAGTATTAATGA 3300  
3241 CAAGCAATTAATTAAGAGTGTCCAGTACTAATGAAGTGGCTCCAGTATTAATGA 3300  
3301 TAGGTTCCAGTATGAAGAAACATTCAGCAGAACTAGTAGAAACAGAGGCGCAAAATGA 3360  
3301 TAGGTTCCAGTATGAAGAAACATTCAGCAGAACTAGTAGAAACAGAGGCGCAAAATGA 3360  
3301 TAGGTTCCAGTATGAAGAAACATTCAGCAGAACTAGTAGAAACAGAGGCGCAAAATGA 3360  
3361 ATGTATAGCTAGTATGAGGTTTGTGCACTGAGTCTAATTAACAAAGTCTTCTGGA 3420  
3361 ATGTATAGCTAGTATGAGGTTTGTGCACTGAGTCTAATTAACAAAGTCTTCTGGA 3420  
3361 ATGTATAGCTAGTATGAGGTTTGTGCACTGAGTCTAATTAACAAAGTCTTCTGGA 3420  
3421 GTATTTGAGCATCTGAAATTAATAAAGCAAGATATGAAGAGTGTGAGTGTG 3480  
3421 GTATTTGAGCATCTGAAATTAATAAAGCAAGATATGAAGAGTGTGAGTGTG 3480  
3421 GTATTTGAGCATCTGAAATTAATAAAGCAAGATATGAAGAGTGTGAGTGTG 3480  
3481 ATACAGATTTCTCTCATATCTGATTCAGATTAAGTAAAGTGTGAGTGTG 3540  
3481 ATACAGATTTCTCTCATATCTGATTCAGATTAAGTAAAGTGTGAGTGTG 3540  
3481 ATACAGATTTCTCTCATATCTGATTCAGATTAAGTAAAGTGTGAGTGTG 3540  
3541 ATGATCTCAGGTTTGTGTCAGACACCTGATGACCTGTTAGATGATGCTAAATTAAG 3600  
3541 ATGATCTCAGGTTTGTGTCAGACACCTGATGACCTGTTAGATGATGCTAAATTAAG 3600

3541 ATGATCTCAGGTTTGTGTCAGACACCTGATGACCTGTTAGATGATGCTAAATTAAG 3600  
3601 AAGATTAAGTATGCTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTAAAGAAAGC 3660  
3601 AAGATTAAGTATGCTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTAAAGAAAGC 3660  
3601 AAGATTAAGTATGCTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTAAAGAAAGC 3660  
3661 TCCAGAAAGAGAGCTTACAGAGAGTCTAGCCCTTACACCATACATTTGGCTAGG 3720  
3661 TCCAGAAAGAGAGCTTACAGAGAGTCTAGCCCTTACACCATACATTTGGCTAGG 3720  
3661 TCCAGAAAGAGAGCTTACAGAGAGTCTAGCCCTTACACCATACATTTGGCTAGG 3720  
3721 GTTACCGAAGAGGCGCAAGAAATTAAGAGTCTCAGAGAGAACTTCTAGAGAGATG 3780  
3721 GTTACCGAAGAGGCGCAAGAAATTAAGAGTCTCAGAGAGAACTTCTAGAGAGATG 3780  
3721 GTTACCGAAGAGGCGCAAGAAATTAAGAGTCTCAGAGAGAACTTCTAGAGAGATG 3780  
3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTTAAAGTAAACATATACCTTCTAGT 3840  
3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTTAAAGTAAACATATACCTTCTAGT 3840  
3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTTAAAGTAAACATATACCTTCTAGT 3840  
3841 CTACTAGGCAATGACACCGTGTCTACCGAGTGTCTGTAAAGAACAGAGAGATTTAT 3900  
3841 CTACTAGGCAATGACACCGTGTCTACCGAGTGTCTGTAAAGAACAGAGAGATTTAT 3900  
3841 CTACTAGGCAATGACACCGTGTCTACCGAGTGTCTGTAAAGAACAGAGAGATTTAT 3900  
3901 TATCATGGAAGATTAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 3960  
3901 TATCATGGAAGATTAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 3960  
3901 TATCATGGAAGATTAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 3960  
3961 AGGAAATCACTTACCTAGTGAAGAAACAAATGCTGCTAGTCTGTTTCTTCAAGTGA 4020  
3961 AGGAAATCACTTACCTAGTGAAGAAACAAATGCTGCTAGTCTGTTTCTTCAAGTGA 4020  
3961 AGGAAATCACTTACCTAGTGAAGAAACAAATGCTGCTAGTCTGTTTCTTCAAGTGA 4020  
3961 AGGAAATCACTTACCTAGTGAAGAAACAAATGCTGCTAGTCTGTTTCTTCAAGTGA 4020  
4021 GTGATTTGGAAGCTTGTACCTGCAATTAACAAACCCAGATCTTCTTGTATGTTCTT 4080  
4021 GTGATTTGGAAGCTTGTACCTGCAATTAACAAACCCAGATCTTCTTGTATGTTCTT 4080  
4021 GTGATTTGGAAGCTTGTACCTGCAATTAACAAACCCAGATCTTCTTGTATGTTCTT 4080  
4021 GTGATTTGGAAGCTTGTACCTGCAATTAACAAACCCAGATCTTCTTGTATGTTCTT 4080  
4081 CCAAAACAAATGAGGCACTGATGAAAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4140  
4081 CCAAAACAAATGAGGCACTGATGAAAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4140  
4081 CCAAAACAAATGAGGCACTGATGAAAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4140  
4081 CCAAAACAAATGAGGCACTGATGAAAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4140  
4141 TTTTCAATGATGAAAGAAAGGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4200  
4141 TTTTCAATGATGAAAGAAAGGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4200  
4141 TTTTCAATGATGAAAGAAAGGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4200  
4141 TTTTCAATGATGAAAGAAAGGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4200  
4201 TGGATTTCAAACTTAAAGTGAAGACATCTGGGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 4260  
4201 TGGATTTCAAACTTAAAGTGAAGACATCTGGGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 4260  
4201 TGGATTTCAAACTTAAAGTGAAGACATCTGGGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 4260  
4201 TGGATTTCAAACTTAAAGTGAAGACATCTGGGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 4260  
4261 ACTGCTCAGGCTATCTCTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4320  
4261 ACTGCTCAGGCTATCTCTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4320  
4261 ACTGCTCAGGCTATCTCTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4320  
4261 ACTGCTCAGGCTATCTCTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4320  
4321 AACATTAACCTGATTAAGGCTCCAGAGAAATGCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4380  
4321 AACATTAACCTGATTAAGGCTCCAGAGAAATGCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4380  
4321 AACATTAACCTGATTAAGGCTCCAGAGAAATGCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4380  
4321 AACATTAACCTGATTAAGGCTCCAGAGAAATGCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4380  
4381 ATGGAGGACGCTTCTTACAGCTACCTTCCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4440  
4381 ATGGAGGACGCTTCTTACAGCTACCTTCCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4440  
4381 ATGGAGGACGCTTCTTACAGCTACCTTCCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4440  
4381 ATGGAGGACGCTTCTTACAGCTACCTTCCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4440  
4441 ACTGCGAATCCAGAAACAAAGCAATCAAGAAAGAGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4500  
4441 ACTGCGAATCCAGAAACAAAGCAATCAAGAAAGAGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4500  
4441 ACTGCGAATCCAGAAACAAAGCAATCAAGAAAGAGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4500  
4441 ACTGCGAATCCAGAAACAAAGCAATCAAGAAAGAGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4500  
4501 GTAAATACCTTATTAAGCAAGATCCAGAAAGGCTTCTGCTGCAAGTGTGAGTGTGAGTGTG 4560  
4501 GTAAATACCTTATTAAGCAAGATCCAGAAAGGCTTCTGCTGCAAGTGTGAGTGTGAGTGTGAGTGTG 4560  
4501 GTAAATACCTTATTAAGCAAGATCCAGAAAGGCTTCTGCTGCAAGTGTGAGTGTGAGTGTGAGTGTG 4560  
4501 GTAAATACCTTATTAAGCAAGATCCAGAAAGGCTTCTGCTGCAAGTGTGAGTGTGAGTGTGAGTGTG 4560  
4561 CAGATAGTCTTACAGTAAATTAAGAAACAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620  
4561 CAGATAGTCTTACAGTAAATTAAGAAACAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620  
4561 CAGATAGTCTTACAGTAAATTAAGAAACAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620  
4561 CAGATAGTCTTACAGTAAATTAAGAAACAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620  
4621 GCCATCATTAAGATGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
4621 GCCATCATTAAGATGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680

```

Db 4621 GCCCATCATAGATGATAGTGGTACATGCCACATTCGCTGGAGTCTTAGAATAGAA 4680
Oy 4681 ACTACCATCTCAAGAGAGAGCTCATTAAGTGTGTGATGTGAGAGAGCACAGCTGGAAG 4740
Db 4681 ACTACCATCTCAAGAGAGAGCTCATTAAGTGTGTGATGTGAGAGAGCACAGCTGGAAG 4740
Oy 4741 AGCTGGGGCCACACGATTTGACGGAACATTTTACTGTCCCAAGCAGAGATCTAGAGGAA 4800
Db 4741 AGCTGGGGCCACACGATTTGACGGAACATTTTACTGTCCCAAGCAGAGATCTAGAGGAA 4800
Oy 4801 CCCCTTACTGATGATCTGGAATCAGCTCTCTCTGTGATGACCTGGAATCTGATCTCTG 4860
Db 4801 CCCCTTACTGATGATCTGGAATCAGCTCTCTCTGTGATGACCTGGAATCTGATCTCTG 4860
Oy 4861 AAGACAGAGCCCCAGAGATCAGCTGTGTGGCAACATACATCTTCAACCTCTGCATTTGA 4920
Db 4861 AAGACAGAGCCCCAGAGATCAGCTGTGTGGCAACATACATCTTCAACCTCTGCATTTGA 4920
Oy 4921 AAGTCCCAATGAAGTGTGCAAAATCTGCCAGAGTCCAGCTGCTGCTCATCTACTG 4980
Db 4921 AAGTCCCAATGAAGTGTGCAAAATCTGCCAGAGTCCAGCTGCTGCTCATCTACTG 4980
Oy 4981 ATACTGCTGGGTATATGATGAGAGAAAGTGTGACAGAGAGAGAGAGAGAGATTTGACAG 5040
Db 4981 ATACTGCTGGGTATATGATGAGAGAAAGTGTGACAGAGAGAGAGAGAGAGATTTGACAG 5040
Oy 5041 CTTCACACAGAAAGGCTACACAAAGAAATGTCATGTGTGTCTGCGCTGACCCAGAG 5100
Db 5041 CTTCACACAGAAAGGCTACACAAAGAAATGTCATGTGTGTCTGCGCTGACCCAGAG 5100
Oy 5101 AATTATGCTGCTGATCAGATTTGCGAAACACACATCATTCTTAATTAATA 5160
Db 5101 AATTATGCTGCTGATCAGATTTGCGAAACACACATCATTCTTAATTAATA 5160
Oy 5161 CTGAAGAGACTACTCATGTGTATGAAAACAGATGCTGATTTGTGTGAGAGAGAGAG 5220
Db 5161 CTGAAGAGACTACTCATGTGTATGAAAACAGATGCTGATTTGTGTGAGAGAGAGAG 5220
Oy 5221 TGAATATTTTCTAGAGATTTGCGGAGAGAAATGGTATGATTTCTGGGTGACCC 5280
Db 5221 TGAATATTTTCTAGAGATTTGCGGAGAGAAATGGTATGATTTCTGGGTGACCC 5280
Oy 5281 AGCTATTTAAAGAAAGAAATGCTGATGATGATGATTTTGAAGTGAAGAGAGATGAG 5340
Db 5281 AGCTATTTAAAGAAAGAAATGCTGATGATGATGATTTTGAAGTGAAGAGAGATGAG 5340
Oy 5341 TCAATGGAAGAAACCAACAGAGTCCAAAGCAGAGAGAGAGATCCACAGAGAGATCT 5400
Db 5341 TCAATGGAAGAAACCAACAGAGTCCAAAGCAGAGAGAGAGATCCACAGAGAGATCT 5400
Oy 5401 TCAGGGGGCTAGAAATCTGTGTGTATGAGGCGCTTACCAACATGSCCAGATCACTGG 5460
Db 5401 TCAGGGGGCTAGAAATCTGTGTGTATGAGGCGCTTACCAACATGSCCAGATCACTGG 5460
Oy 5461 AATGATGATGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5520
Db 5461 AATGATGATGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5520
Oy 5521 GCACAGAGTGTCCACCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5580
Db 5521 GCACAGAGTGTCCACCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5580
Oy 5581 TCCATGCAATTTGGGAGAGATGTGTGAGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5640
Db 5581 TCCATGCAATTTGGGAGAGATGTGTGAGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5640
Oy 5641 GTGTAGACACTTACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5700
Db 5641 GTGTAGACACTTACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5700
Oy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

```

```

RESULT 10
ID T18310
AC T18310; standard; cDNA; 5914 BP.
DT 05-JUN-1996 (first entry)
DE BRCA1, Breast and ovarian cancer predisposing gene.
KW BRCA1; Breast cancer; ovarian cancer; predisposing gene;
susceptibility gene; diagnosis; prognosis; gene therapy; ds.
OS Homo sapiens.
FH Key location/Qualifiers
FT cds 120..5711
FT
FT MO9605307-A2.
FT 22-FEB-1996.
FT 11-AUG-1995; US-289221.
FT 12-AUG-1994; US-289221.
FT 02-SEP-1994; US-300266.
FT 16-SEP-1994; US-308104.
FT 29-NOV-1994; US-348824.
FT 24-MAR-1995; US-409305.
FT 07-JUN-1995; US-488011.
FT 07-JUN-1995; US-483554.
FT 07-JUN-1995; US-487002.
FT (MIR-) MIRIAD GENETICS INC.
FT (UTAH ) UNIV UTAH RES FOUND.
FT (USH ) US DEPT HEALTH & HUMAN SERVICES.
FT Futrell AP, Goldgar DE, Harsman KD, Kamb A, Miki Y;
PI Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV;
PI Wiseman RM;
DR WPI; 96-139703/14.
DR P-SDB; R91208.
PT New isolated human cancer predisposing gene, BRCA1 - used to develop
PT prods. for diagnosis, prognosis and therapy of cancers, partic.
PT breast and ovarian cancers
PS Claim 2: Page 108-117; 190pp; English.
CC The breast and ovarian cancer susceptibility gene, BRCA1, was
CC identified. 4 kindred families provided genetic evidence for
CC localisation of BRCA1 to a sufficiently small region for the appln.
CC of positional cloning strategies. A detailed map of transcripts was
CC developed for the region of 17q21 between D17S1321 and D17S1324. A
CC combination of sequences obt'd. from cDNA clones, hybrid-selected
CC sequences and PCR prods. allowed construction of a composite full-
CC length BRCA1 cDNA (T18310). A genomic sequence (T18325) was also obt'd.
CC Certain alleles of BRCA1 (see T18311-14) predispose an individual to
CC develop cancer. The isolated cDNA is used in methods for either
CC diagnosis of the predisposition to cancer (partic. breast and ovarian
CC cancer), or for the diagnosis or prognosis of cancer, and also in
CC gene-based therapies directed at cancer cells.
SQ Sequence 5914 BP; 2006 A; 1156 C; 1316 G; 1436 T;

Query Match 100.0%; Score 5709.4; DB 1; Length 5914;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AGCTGCTGAGACTTCTGACCCGACACAGAGCTGTGGGTTTCTCAGATTAAGTGGCC 60
Db 1 AGCTGCTGAGACTTCTGACCCGACACAGAGCTGTGGGTTTCTCAGATTAAGTGGCC 60
Oy 61 CCTGGCCTCAGAGAGGCTTACCTCTGCTGTGGGTAAGTTCATTGGAAGAGAA 120
Db 61 CCTGGCCTCAGAGAGGCTTACCTCTGCTGTGGGTAAGTTCATTGGAAGAGAA 120
Oy 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTCAAAATGCTAATTAATCTAGCAAAA 180
Db 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTCAAAATGCTAATTAATCTAGCAAAA 180
Oy 181 TCTTAGAGTGTCCATCTCTGAGATTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240
Db 181 TCTTAGAGTGTCCATCTCTGAGATTGATCAAGAACTGTCTCTCCCAAAAGTGTGACC 240

```

```
QY 241 ACATATTTGCAATTTTGCATGCTGAAACCTTCTCAACAGAAAGAGGGCTTCAAGT 300
| | | | |
Db 241 ACATATTTGCAATTTTGCATGCTGAAACCTTCTCAACAGAAAGAGGGCTTCAAGT 300
QY 301 GTCCCTTATGTAAGATGATATAACCAAAAAGAGCCTACAGAAAGTACGAGATTAGTC 360
| | | | |
Db 301 GTCCCTTATGTAAGATGATATAACCAAAAAGAGCCTACAGAAAGTACGAGATTAGTC 360
QY 361 AACTTGTGAAGAGCCTATGTAAGATGATGCTTGTTCAGCTTACAGAGGTTGGAGT 420
| | | | |
Db 361 AACTTGTGAAGAGCCTATGTAAGATGATGCTTGTTCAGCTTACAGAGGTTGGAGT 420
QY 421 ATGCAACACGCTATATTTTGCACAAAAAGAAATTAACCTCTCCGAACTCTAAAGATG 480
| | | | |
Db 421 ATGCAACACGCTATATTTTGCACAAAAAGAAATTAACCTCTCCGAACTCTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCACAAAAGCTTCTACAGAGT 540
| | | | |
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCACAAAAGCTTCTACAGAGT 540
QY 541 AACCAGAAAACTCTTCTCTGAGAGAAACAGCTCTCAGTGTCCAACTCTAAACCTTGGAA 600
| | | | |
Db 541 AACCAGAAAACTCTTCTCTGAGAGAAACAGCTCTCAGTGTCCAACTCTAAACCTTGGAA 600
QY 601 CTGTGAAACTCTGAGAGCAAAAGAGGGGATACAACTCTCAAAAAGAGCTGTCTACATTG 660
| | | | |
Db 601 CTGTGAAACTCTGAGAGCAAAAGAGGGGATACAACTCTCAAAAAGAGCTGTCTACATTG 660
QY 661 AATTGGGATCTGATCTTCTGAGAGATACCGTTAATAAGCAACTTATTTGAGTGGAG 720
| | | | |
Db 661 AATTGGGATCTGATCTTCTGAGAGATACCGTTAATAAGCAACTTATTTGAGTGGAG 720
QY 721 ATCAAGAAATTTGTAACAATAACACCCCTCAAGAACCAAGGATGAATCATGTTGGATTCTG 780
| | | | |
Db 721 ATCAAGAAATTTGTAACAATAACACCCCTCAAGAACCAAGGATGAATCATGTTGGATTCTG 780
QY 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGAGGATGTAACAAATCTGAACATCATATCAAC 840
| | | | |
Db 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGAGGATGTAACAAATCTGAACATCATATCAAC 840
QY 841 CCAATTAATTAATGATTTTGAACACCACTAGAGAGCGTGCAGCTGAGAGGCTACAGAAAAAGT 900
| | | | |
Db 841 CCAATTAATTAATGATTTTGAACACCACTAGAGAGCGTGCAGCTGAGAGGCTACAGAAAAAGT 900
QY 901 ATCAGGGTACTTCTGTTTCAAACTTGATGATGAGGACCATGTGGCAAAATACTATGCCA 960
| | | | |
Db 901 ATCAGGGTACTTCTGTTTCAAACTTGATGATGAGGACCATGTGGCAAAATACTATGCCA 960
QY 961 GCTCATTACAGCATGAGAACAGCAGTTTATTTACTACTAAAGACAGATGATAGTACAAA 1020
| | | | |
Db 961 GCTCATTACAGCATGAGAACAGCAGTTTATTTACTACTAAAGACAGATGATAGTACAAA 1020
QY 1021 AGGCTGAATCTGTAATTAAGCAAAACAGCCTGAGCTTAGCAGAGGACCAATTAACAGAT 1080
| | | | |
Db 1021 AGGCTGAATCTGTAATTAAGCAAAACAGCCTGAGCTTAGCAGAGGACCAATTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAGAAACATGTATATAGCGGACTCCAGCAGCAAGAAAAAGGTAG 1140
| | | | |
Db 1081 GGGCTGGAAGTAAGAAACATGTATATAGCGGACTCCAGCAGCAAGAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGGAATAGCAGAAACTGCCATGCT 1200
| | | | |
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGGAATAGCAGAAACTGCCATGCT 1200
QY 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCCCTTGGATACACTAAATAGCAGCTTACAG 1260
| | | | |
Db 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCCCTTGGATACACTAAATAGCAGCTTACAG 1260
QY 1261 AAGTTAATGAGTGGTTTCCAGAAAGTATGAATGTTAGGTTCTGATGACTCAGATGATG 1320
| | | | |
Db 1261 AAGTTAATGAGTGGTTTCCAGAAAGTATGAATGTTAGGTTCTGATGACTCAGATGATG 1320
QY 1321 GGGAGTGTGAATCAAAATGCCAAAGTACGTATGATTGGACGTTCTAAATGAGGTAGATG 1380
| | | | |
QY 1321 GGGAGTGTGAATCAAAATGCCAAAGTACGTATGATTGGACGTTCTAAATGAGGTAGATG 1380
| | | | |
Db 1321 GGGAGTGTGAATCAAAATGCCAAAGTACGTATGATTGGACGTTCTAAATGAGGTAGATG 1380
| | | | |
QY 1381 AATATCTGTTCTTCCAGAAAAATAGACTTACTGGCCAGTATCCATGAGGCTTTAA 1440
| | | | |
Db 1381 AATATCTGTTCTTCCAGAAAAATAGACTTACTGGCCAGTATCCATGAGGCTTTAA 1440
QY 1441 TATGTAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATTGAAAGACAAATAT 1500
| | | | |
Db 1441 TATGTAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATTGAAAGACAAATAT 1500
QY 1501 TTGGGAAAACCTTACGGAAGAGCAAGCCTCCCAACTTAAGCAGTATACGTAATATC 1560
| | | | |
Db 1501 TTGGGAAAACCTTACGGAAGAGCAAGCCTCCCAACTTAAGCAGTATACGTAATATC 1560
QY 1561 TAAATATAGAGCATTTGTTACTGAGCCACAGATTAATACAAAGAGCGTCCCTCCAAATA 1620
| | | | |
Db 1561 TAAATATAGAGCATTTGTTACTGAGCCACAGATTAATACAAAGAGCGTCCCTCCAAATA 1620
QY 1621 AATTAAAGCGTAAAGAGAGCTACATCAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680
| | | | |
Db 1621 AATTAAAGCGTAAAGAGAGCTACATCAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTCAAAAAGACTCTGTAATGATTAATCAGGAACTTAACCAACGAGAGC 1740
| | | | |
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCTGTAATGATTAATCAGGAACTTAACCAACGAGAGC 1740
QY 1741 AGAATGGTCAAGTATGAATATTACTAATAGTGTGTCAGTAATTAACCAAGAGTATT 1800
| | | | |
Db 1741 AGAATGGTCAAGTATGAATATTACTAATAGTGTGTCAGTAATTAACCAAGAGTATT 1800
QY 1801 CTATTCGAATGAGAAAAATCTTAACCAATAGAAATCTCTGAAAAAGAAATCTGCTTTCA 1860
| | | | |
Db 1801 CTATTCGAATGAGAAAAATCTTAACCAATAGAAATCTCTGAAAAAGAAATCTGCTTTCA 1860
QY 1861 AAACGAAAGCTGAACCTATTAAGAGCAGTAAAGCAATATGGAATCTGAATTAATATCC 1920
| | | | |
Db 1861 AAACGAAAGCTGAACCTATTAAGAGCAGTAAAGCAATATGGAATCTGAATTAATATCC 1920
QY 1921 ACAATTCAAAAGACCTTAATAAGAAATAGGCTGAGAGGAAGTCTTCTACAGGCAATATTC 1980
| | | | |
Db 1921 ACAATTCAAAAGACCTTAATAAGAAATAGGCTGAGAGGAAGTCTTCTACAGGCAATATTC 1980
QY 1981 ATGCGCTTGAAGTATGATAGTAAAGATTAAGCCCACTTAATGTAATGTAATTCGAA 2040
| | | | |
Db 1981 ATGCGCTTGAAGTATGATAGTAAAGATTAAGCCCACTTAATGTAATGTAATTCGAA 2040
QY 2041 TTGATAGTGTCTTACAGCTGGAAGAGATTAAGAAAAAGTACCAACCAATGCGAGTCA 2100
| | | | |
Db 2041 TTGATAGTGTCTTACAGCTGGAAGAGATTAAGAAAAAGTACCAACCAATGCGAGTCA 2100
QY 2101 GGCACAGCAGAAACCTTAACAATCATGGAAGGTAAGAACTGGAACCTGAGGAGCAAGAGA 2160
| | | | |
Db 2101 GGCACAGCAGAAACCTTAACAATCATGGAAGGTAAGAACTGGAACCTGAGGAGCAAGAGA 2160
QY 2161 GTAACAAAGCCAAATGAACAGACAAAGTAAAGAGACATGACAGCTACTTTCCAGAGCTGA 2220
| | | | |
Db 2161 GTAACAAAGCCAAATGAACAGACAAAGTAAAGAGACATGACAGCTACTTTCCAGAGCTGA 2220
QY 2221 AGTTAACAATGACACCTGGTCTTTACTAAGTGTCCAATACCAGTGAATTAAGAAAT 2280
| | | | |
Db 2221 AGTTAACAATGACACCTGGTCTTTACTAAGTGTCCAATACCAGTGAATTAAGAAAT 2280
QY 2281 TTGTCAATCTTACCTTCCAGAGAGAAAAAAGAGAACTAGAAACGTTAAAGGTG 2340
| | | | |
Db 2281 TTGTCAATCTTACCTTCCAGAGAGAAAAAAGAGAACTAGAAACGTTAAAGGTG 2340
QY 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAGGTTTTCAGAACTG 2400
| | | | |
Db 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAGGTTTTCAGAACTG 2400
QY 2401 AAAGATCTGTAGAGATGACAGTATTTCAATGTTACTGCTACTGATTAATGAGCTCAGG 2460
| | | | |
Db 2401 AAAGATCTGTAGAGATGACAGTATTTCAATGTTACTGCTACTGATTAATGAGCTCAGG 2460
| | | | |
```



Db 2401 AAGATCTGTAGAGTAGCAGATATTTCATTGGTACTGGTGTGANTTANGGCACTAGG 2460  
QY 2461 AAGATATCTGTTACTGGAAGTTAGCACTGTAGGGAAGGCAAAAACGAACCAATTAAT 2520  
Db 2461 AAGATATCTGTTACTGGAAGTTAGCACTGTAGGGAAGGCAAAAACGAACCAATTAAT 2520  
QY 2521 GTGTGAGTCAAGTGTGCAAGCATTTGAAAAACCCCAAGGACTAATTCATGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGTGCAAGCATTTGAAAAACCCCAAGGACTAATTCATGTTGTTCCAAAG 2580  
QY 2581 ATATATGAATATGACACGAAGGCTTTAATGATATCCATTGGGACATGAATTAACCAAGTC 2640  
Db 2581 ATATATGAATATGACACGAAGGCTTTAATGATATCCATTGGGACATGAATTAACCAAGTC 2640  
QY 2641 GGGAAACAAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTAGTATTTGCAAGTACAT 2700  
Db 2641 GGGAAACAAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTAGTATTTGCAAGTACAT 2700  
QY 2701 TCAAGGTTTCAAAAGCCGCACTATTTGCTGTTTCAAAATCCGAAATGCAAGAGAG 2760  
Db 2701 TCAAGGTTTCAAAAGCCGCACTATTTGCTGTTTCAAAATCCGAAATGCAAGAGAG 2760  
QY 2761 AATGTGCAACATTTCTGCCCACCTGCTGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCCCACCTGCTGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGGAAGAAATATCAAGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGGAAGAAATATCAAGAAAGATGAGTCTAATATCAAGCCTGTAC 2880  
QY 2881 AGACATTTATATACACTGCGAGGCTTCCCTGCTGTTGTCAGAAAGATTAAGCACTGATA 2940  
Db 2881 AGACATTTATATACACTGCGAGGCTTCCCTGCTGTTGTCAGAAAGATTAAGCACTGATA 2940  
QY 2941 ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
QY 3001 ACGAAACTGCACTATTTACTCCAAATTAACATGACCTTTTACAAACCCATATCCTATAC 3060  
Db 3001 ACGAAACTGCACTATTTACTCCAAATTAACATGACCTTTTACAAACCCATATCCTATAC 3060  
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAATTAATGAAGAAATCTGCTAGAG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAATTAATGAAGAAATCTGCTAGAG 3120  
QY 3121 AAAAATTTGAGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACATTTCAA 3180  
Db 3121 AAAAATTTGAGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACATTTCAA 3180  
QY 3181 GTACAGTGAAGCAATTAAGCCGTAAATGTAGAGAAAAATGTTTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAAGCAATTAAGCCGTAAATGTAGAGAAAAATGTTTTTAAAGAGCCAGCT 3240  
QY 3241 CAAGCAATATTAATGAAGTGTTCAGTACTAATGAAGGGGCTCCAGTATTAAGTAA 3300  
Db 3241 CAAGCAATATTAATGAAGTGTTCAGTACTAATGAAGGGGCTCCAGTATTAAGTAA 3300  
QY 3301 TAGGTTCCAGTGTGAAGAACATTCAGCAGACTAGTAGAAACAGAGGCGCAAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGTGAAGAACATTCAGCAGACTAGTAGAAACAGAGGCGCAAAATTTGA 3360  
QY 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTATTAACAAAGTCTTCTGGA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTATTAACAAAGTCTTCTGGA 3420  
QY 3421 GTAATGTAGACATCTCTGAATTAAGAAATGAAGAAATGAAGAGTGTTCAGACTGTA 3480  
Db 3421 GTAATGTAGACATCTCTGAATTAAGAAATGAAGAAATGAAGAGTGTTCAGACTGTA 3480  
QY 3481 ATACAGATTTCTCTCATAATCTGATTTAGATTAAGTAAAGCAAGCCTATGGGAAGTATC 3540  
Db 3481 ATACAGATTTCTCTCATAATCTGATTTAGATTAAGTAAAGCAAGCCTATGGGAAGTATC 3540

---

QY 3541 ATGCATCTCAGGTTTGTCTTGAGACACCTGATAGCTGTTAGATGATGTAATTAAGC 3600  
Db 3541 ATGCATCTCAGGTTTGTCTTGAGACACCTGATAGCTGTTAGATGATGTAATTAAGC 3600  
QY 3601 AAGTACTAGTTTGTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTTTACCAAAAGC 3660  
Db 3601 AAGTACTAGTTTGTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTTTACCAAAAGC 3660  
QY 3661 TCCGAAGAGAGAGCTTAGCAGAGTCTTCCAGTCTTCAACCCATACATTTGGCTCAG 3720  
Db 3661 TCCGAAGAGAGAGCTTAGCAGAGTCTTCCAGTCTTCAACCCATACATTTGGCTCAG 3720  
QY 3721 GTTACCGAAGAGGCGCCAGAAATTAAGAGTCTCAGAGAGAACTTATCTAGTAGAGATG 3780  
Db 3721 GTTACCGAAGAGGCGCCAGAAATTAAGAGTCTCAGAGAGAACTTATCTAGTAGAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAACTGTTGTTATTTGTTAAATTAACATTAACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAACTGTTGTTATTTGTTAAATTAACATTAACCTTCTCAGT 3840  
QY 3841 CTACTAGGCAATAGCACCGTTGCTACGAGTGTCTGTAAGAAACACAGAGAGAAATTTAT 3900  
Db 3841 CTACTAGGCAATAGCACCGTTGCTACGAGTGTCTGTAAGAAACACAGAGAGAAATTTAT 3900  
QY 3901 TATCATTAAGAAATAGCTTAATGACTGACAGTAAACAGGATTAATTTGCAAGGATCTC 3960  
Db 3901 TATCATTAAGAAATAGCTTAATGACTGACAGTAAACAGGATTAATTTGCAAGGATCTC 3960  
QY 3961 AGGAACATCAACCTTAGTGAGGAAGAAATGTTCTGCTAGTCTTTTCTTCTACAGTCA 4020  
Db 3961 AGGAACATCAACCTTAGTGAGGAAGAAATGTTCTGCTAGTCTTTTCTTCTACAGTCA 4020  
QY 4021 GTGAATTTGAGAGCTTGACTGCAATATCAAAACCCAGAGATCTTCTGATGTTGTTCT 4080  
Db 4021 GTGAATTTGAGAGCTTGACTGCAATATCAAAACCCAGAGATCTTCTGATGTTGTTCT 4080  
QY 4081 CCAACCAATGAGGCAATCACTGTGAAGCCAGGAGTGTGCTGAGTGCACAAAGAAATGG 4140  
Db 4081 CCAACCAATGAGGCAATCACTGTGAAGCCAGGAGTGTGCTGAGTGCACAAAGAAATGG 4140  
QY 4141 TTTCAGATGATGAAGAAAGAGAGGCGTTGGAAGAAATTAATCAAGAGAGCAACCA 4200  
Db 4141 TTTCAGATGATGAAGAAAGAGAGGCGTTGGAAGAAATTAATCAAGAGAGCAACCA 4200  
QY 4201 TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGCCTCTGAG 4260  
Db 4201 TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGCCTCTGAG 4260  
QY 4261 ACTGCTCAGGCGTATCTCTCAGAGTGAATTTTAAACACTCAGCAGAGGATACCATGC 4320  
Db 4261 ACTGCTCAGGCGTATCTCTCAGAGTGAATTTTAAACACTCAGCAGAGGATACCATGC 4320  
QY 4321 AACATTAACCTGAATGAAGGCTCCAGAGAAATGGCTGAATAGAGTGTGTAAGAACGC 4380  
Db 4321 AACATTAACCTGAATGAAGGCTCCAGAGAAATGGCTGAATAGAGTGTGTAAGAACGC 4380  
QY 4381 ATGGAGCCAGCCTTTTAAACAGCTTACCTTCCATTAAGTACCTTTGCTGCTTGAGG 4440  
Db 4381 ATGGAGCCAGCCTTTTAAACAGCTTACCTTCCATTAAGTACCTTTGCTGCTTGAGG 4440  
QY 4441 ACCTGCGAAATCCAGAACAAAGCACATCAAGAAAAGCAGTATTAACCTTACAGAAAAGTA 4500  
Db 4441 ACCTGCGAAATCCAGAACAAAGCACATCAAGAAAAGCAGTATTAACCTTACAGAAAAGTA 4500  
QY 4501 GTGAATACCTTAATGAAGCAGAAATCCAGAGGCGTTTCTGCTGACAAAGTTGAGGCTG 4560  
Db 4501 GTGAATACCTTAATGAAGCAGAAATCCAGAGGCGTTTCTGCTGACAAAGTTGAGGCTG 4560  
QY 4561 CAGATAGTTCTACAGATTAAGAAATGAAGAGCAGAGTGAAGAGTCAATCCCTTAAAT 4620  
Db 4561 CAGATAGTTCTACAGATTAAGAAATGAAGAGCAGAGTGAAGAGTCAATCCCTTAAAT 4620



```

QY 4621 GCCCATCATAGATGATAGTGTGTACATGACAGTGTCTGTGGAGATCTTCAGAAATAGAA 4680
    |||||||
Db 4621 GCCCATCATAGATGATAGTGTGTACATGACAGTGTCTGTGGAGATCTTCAGAAATAGAA 4680
QY 4681 ACTACCATCTCTCAAGAGAGAGAGCTCATTAAGGTTGTGTATGTGAGAGAGACAAGCTGGAAG 4740
    |||||||
Db 4681 ACTACCATCTCTCAAGAGAGAGAGCTCATTAAGGTTGTGTATGTGAGAGAGACAAGCTGGAAG 4740
QY 4741 AGTCTGGGCGACAGATTTGACGAAACATCTTACTTCCAGAGGCAAGATCTAGAGGAA 4800
    |||||||
Db 4741 AGTCTGGGCGACAGATTTGACGAAACATCTTACTTCCAGAGGCAAGATCTAGAGGAA 4800
QY 4801 CCCCCTACCTGGAAATGTGAATAGGCTCTTCTGTATGACCTGATCTGATCTTCTG 4860
    |||||||
Db 4801 CCCCCTACCTGGAAATGTGAATAGGCTCTTCTGTATGACCTGATCTGATCTTCTG 4860
QY 4861 AAGACAGAGCCCCAGAGATCGCTGTTGGCAACATACCATTTCAACCTCTGCATTTGA 4920
    |||||||
Db 4861 AAGACAGAGCCCCAGAGATCGCTGTTGGCAACATACCATTTCAACCTCTGCATTTGA 4920
QY 4921 AAGTTCCTCCAAATTTGAAAGTTGCGAAATCTGCCCCAGAGTCCAGTCTCATACTG 4980
    |||||||
Db 4921 AAGTTCCTCCAAATTTGAAAGTTGCGAAATCTGCCCCAGAGTCCAGTCTCATACTG 4980
QY 4981 ATACTCTGGGTATATGCAATGAAAGAAAGTGTGACGAGGAGAAAGCCAGAAATGACAG 5040
    |||||||
Db 4981 ATACTCTGGGTATATGCAATGAAAGAAAGTGTGACGAGGAGAAAGCCAGAAATGACAG 5040
QY 5041 CTTCACAGAGAAAGGTCACAAAGAAATGTCATGGTGGTGTGCTGGCTGACCCAGAG 5100
    |||||||
Db 5041 CTTCACAGAGAAAGGTCACAAAGAAATGTCATGGTGGTGTGCTGGCTGACCCAGAG 5100
QY 5101 AATTATGCTGCTGTACAAAGTTTGCAGAAACACCAACATCACTTAATCTAATTA 5160
    |||||||
Db 5101 AATTATGCTGCTGTACAAAGTTTGCAGAAACACCAACATCACTTAATCTAATTA 5160
QY 5161 CTGAAAGAGCTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGAAACGAGAC 5220
    |||||||
Db 5161 CTGAAAGAGCTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGAAACGAGAC 5220
QY 5221 TGAATATTTTCTAGAAATTTGCGGAGAGAAATGGTAGTACTTATTTCTGGGTGACC 5280
    |||||||
Db 5221 TGAATATTTTCTAGAAATTTGCGGAGAGAAATGGTAGTACTTATTTCTGGGTGACC 5280
QY 5281 AGCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG 5340
    |||||||
Db 5281 AGCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG 5340
QY 5341 TCATATGGAAGAAACCAAGGTCACAAAGGAGACAGAGAAATCCGAGACAGAAATCT 5400
    |||||||
Db 5341 TCATATGGAAGAAACCAAGGTCACAAAGGAGACAGAGAAATCCGAGACAGAAATCT 5400
QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCACCAACATGCCACAGATCAATGG 5460
    |||||||
Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCACCAACATGCCACAGATCAATGG 5460
QY 5461 AATGATGATGATGAGTGTGTGTGCTGCTGTGTGTAAGAGAGCTTTTCATTCACCTTG 5520
    |||||||
Db 5461 AATGATGATGAGTGTGTGTGCTGCTGTGTGTAAGAGAGCTTTTCATTCACCTTG 5520
QY 5521 GCACAGAGTGTCCACCAATTTGTTGTGTGACAGCCAGATGCTTGACAGAGAGATGGCT 5580
    |||||||
Db 5521 GCACAGAGTGTCCACCAATTTGTTGTGTGACAGCCAGATGCTTGACAGAGATGGCT 5580
QY 5581 TCATATGCAATTTGGGAGATGTGTGAGGACACCTGTGGTGAACCCAGAGTGGGTTTGACA 5640
    |||||||
Db 5581 TCATATGCAATTTGGGAGATGTGTGAGGACACCTGTGGTGAACCCAGAGTGGGTTTGACA 5640
QY 5641 GTGTAGCACTCTACAGATGTCAGAGAGAGCTGACACCTACCTGATACCCAGATCCCCACA 5700
    |||||||
Db 5641 GTGTAGCACTCTACAGATGTCAGAGAGAGCTGACACCTACCTGATACCCAGATCCCCACA 5700
QY 5701 GGCACACTACTGA 5711

```

```

Db 5701 GGCACACTACTGA 5711
    |||||||
RESULT 11
ID T17438 standard; cDNA: 5914 BP.
AC T17438;
DT 30-SEP-1996 (first entry)
DE BRCA1 coding sequence.
KW Cancer therapy: breast and ovarian cancer predisposing gene; immunogen;
   antibody production; germline alteration; probe; lesion neoplasia; human;
   gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
OS Homo sapiens.
FH key Location/Qualifiers
FT cds 120..5711
FT /tag= a
FT /product= BRCA1
PN MO9605306-A2.
PD 22-FEB-1996.
PE 11-AUG-1995; U10202.
PR 12-AUG-1994; US-289221.
PR 02-SEP-1994; US-300266.
PR 16-SEP-1994; US-308104.
PR 29-NOV-1994; US-348824.
PR 24-MAR-1995; US-409305.
PR 07-JUN-1995; US-483553.
PR 07-JUN-1995; US-480784.
PA (MYRI-) MYRIAD GENETICS INC.
PA (CANC-) CANCER INST.
PA (RECH-) CENT RECH DU CHUL.
PI Durocher F, Eml M, Nakamura Y, Simard J, Shattuck-Eidens DM;
DR P-PSDB; R81481.
PT New nucleic acid and polypeptide for mutant or polymorphic BRCA1
   gene - for diagnosis and therapy of human breast and ovarian cancer
   and for diagnosing pre-disposition to these cancers
PS Claim 1; Page 119-128; 218pp; English.
CC This sequence represents the cDNA of the human breast and ovarian cancer
   predisposing gene (BRCA1). Proteins encoded by mutations of this
   sequence (see T17439-T17453 and T17455-T17529) can be used as immunogens
   for antibody production. An additional BRCA1 mutant, with a T to G
   mutation and 59 nucleotide insert (encoding a protein which terminates at
   residue 75) is also claimed, however the exact location of the mutations
   is not specified so the sequence could not be created. The mutant BRCA1
   sequence have at least 1 mutation or polymorphism in comparison to this
   sequence. By detecting a germline alteration in this gene, a
   predisposition for breast and ovarian cancer can be diagnosed. In one
   method, BRCA1 mRNA isolated from a tissue sample from a subject has a
   allele-specific probe for a mutation of this sequence (or an
   conditions allow for hybridisation of the probe to the mRNA, and any
   hybridisation which occurs is detected. Alternatively, the BRCA1 gene in
   the tissue sample is isolated, and a shift in electrophoretic mobility of
   single stranded DNA from the sample on a non-denaturing polyacrylamide
   gel indicates a mutation. These methods of detection can also diagnose a
   CC lesion neoplasia associated with the BRCA1 locus. The methods may be
   used in gene therapy, protein replacement therapy and protein mimetics,
   CC and may be used to screen for drugs in cancer therapy.
SQ Sequence 5914 BP; 2006 A; 1156 C; 1316 G; 1436 T;

```

```

Query Match 100.0%; Score 5709.4; DB 1; Length 5914;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 AGCTGCTAGACTCTCTGAGCCCGCACACAGGCTGTGGGGTTCTTCAGATTAAGTGGCC 60
    |||||||
Db 1 AGCTGCTAGACTCTCTGAGCCCGCACACAGGCTGTGGGGTTCTTCAGATTAAGTGGCC 60
QY 61 CCTGGCCTAGAGAGGCTTCCACCTCTGCTGGGTAAGTTCATTGGAACAGAAAGAAA 120
    |||||||
Db 61 CCTGGCCTAGAGAGGCTTCCACCTCTGCTGGGTAAGTTCATTGGAACAGAAAGAAA 120

```

OY 121 TGGATTATCTGCTCTCCGCTTGGAAGACTACAAAAATGTCATTAATGCTATGACAGAAAA 180  
| | | | |  
Db 121 TGGATTATCTGCTCTCCGCTTGGAAGACTACAAAAATGTCATTAATGCTATGACAGAAAA 180  
OY 181 TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGCTCCACAAAGGTACC 240  
| | | | |  
Db 181 TCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGCTCCACAAAGGTACC 240  
OY 241 ACATATTTTGC AAAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGGCCTTACAGT 300  
| | | | |  
Db 241 ACATATTTTGC AAAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGGCCTTACAGT 300  
OY 301 GTCCCTTATGTAAGATGATATACCAAAAGAGCCTACAGAAAGTACAGATTTAGTC 360  
| | | | |  
Db 301 GTCCCTTATGTAAGATGATATACCAAAAGAGCCTACAGAAAGTACAGATTTAGTC 360  
OY 361 AACCTGTGAAGAGCTATGAAATCATTTGTGCTTTGACGTTCACAGAGTTTGAGT 420  
| | | | |  
Db 361 AACCTGTGAAGAGCTATGAAATCATTTGTGCTTTGACGTTCACAGAGTTTGAGT 420  
OY 421 ATGCAAAACGCTATATATTTTGC AAAAATATACCTCTCCGTAACATCTAAAAGATG 480  
| | | | |  
Db 421 ATGCAAAACGCTATATATTTTGC AAAAATATACCTCTCCGTAACATCTAAAAGATG 480  
OY 481 AAGTTTCTATCATCCAAAGTATGAGGCTACAGAAACCGTCCAAAAGACTTCTACAGATG 540  
| | | | |  
Db 481 AAGTTTCTATCATCCAAAGTATGAGGCTACAGAAACCGTCCAAAAGACTTCTACAGATG 540  
OY 541 AACCCGAAAATCTCTCCCTGACAGAAACAGTCTCAAGTGTCCAACTCTCAACCTTGGA 600  
| | | | |  
Db 541 AACCCGAAAATCTCTCCCTGACAGAAACAGTCTCAAGTGTCCAACTCTCAACCTTGGA 600  
OY 601 CTGTGAGAACTCTGAGAGCAAAAGCAGGATACAACTTCAAAAAGAGTCTGTACATTG 660  
| | | | |  
Db 601 CTGTGAGAACTCTGAGAGCAAAAGCAGGATACAACTTCAAAAAGAGTCTGTACATTG 660  
OY 661 AATGGGATTCGATCTCTGTAAGATACCGTTATTAAGCACTTATTGCAAGTGGAG 720  
| | | | |  
Db 661 AATGGGATTCGATCTCTGTAAGATACCGTTATTAAGCACTTATTGCAAGTGGAG 720  
OY 721 ATCAAGATTTGTTACAAATCACCCCTCAAGAAACAGGGATGAAATCAGTTTGGATTCTG 780  
| | | | |  
Db 721 ATCAAGATTTGTTACAAATCACCCCTCAAGAAACAGGGATGAAATCAGTTTGGATTCTG 780  
OY 781 CAAAAAGGCTGCTGTGTAATTTCTGAGACGGATGTAACTGAACATCATCAAC 840  
| | | | |  
Db 781 CAAAAAGGCTGCTGTGTAATTTCTGAGACGGATGTAACTGAACATCATCAAC 840  
OY 841 CCAGTAAATTAATGTTTGAACACCACTGAGAAAGCTGACAGTGGCAAAATACATGCA 900  
| | | | |  
Db 841 CCAGTAAATTAATGTTTGAACACCACTGAGAAAGCTGACAGTGGCAAAATACATGCA 900  
OY 901 ATCAGGAGTGTCTGTTCAAACTTGCAATGTCAGTGTGAGCAGTGTGCAAAATPCTCATGCCA 960  
| | | | |  
Db 901 ATCAGGAGTGTCTGTTCAAACTTGCAATGTCAGTGTGAGCAGTGTGCAAAATPCTCATGCCA 960  
OY 961 GCTCATTTACACATGAGAACAGCACTTTATCTACTCAATAAGACAGAAATGATGAAA 1020  
| | | | |  
Db 961 GCTCATTTACACATGAGAACAGCACTTTATCTACTCAATAAGACAGAAATGATGAAA 1020  
OY 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCCTGGCTTACCAAGAGGCCAACTAACAGT 1080  
| | | | |  
Db 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCCTGGCTTACCAAGAGGCCAACTAACAGT 1080  
OY 1081 GGGCTGGAAGTAAAGAAACATGATGATGAGCGGACTCCAGCAGAGAAAAAGGTAG 1140  
| | | | |  
Db 1081 GGGCTGGAAGTAAAGAAACATGATGATGAGCGGACTCCAGCAGAGAAAAAGGTAG 1140  
OY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGAGAAACTGCCATGCT 1200  
| | | | |  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGAGAAACTGCCATGCT 1200

OY 1201 CAGAGAACTCTAGAGATPACTGAAGATGTTCTTGATTAACACTAAATAGCAGCACTCAGA 1260  
| | | | |  
Db 1201 CAGAGAACTCTAGAGATPACTGAAGATGTTCTTGATTAACACTAAATAGCAGCACTCAGA 1260  
OY 1261 AAGTTAATGAGTGGTTTTCAGAAAGTGAAGCACTGTTAGTCTGATGCTACATGATG 1320  
| | | | |  
Db 1261 AAGTTAATGAGTGGTTTTCAGAAAGTGAAGCACTGTTAGTCTGATGCTACATGATG 1320  
OY 1321 GGGAGTCTGAATCAAAATGGCAAAAGTATGATGATTTGAGCCTTCAATATGAGTAGATG 1380  
| | | | |  
Db 1321 GGGAGTCTGAATCAAAATGGCAAAAGTATGATGATTTGAGCCTTCAATATGAGTAGATG 1380  
OY 1381 AATATCTGCTTCTTACAGAAAAATAGACTTACTGGCCAGTATCCTCATGAGCCTTAA 1440  
| | | | |  
Db 1381 AATATCTGCTTCTTACAGAAAAATAGACTTACTGGCCAGTATCCTCATGAGCCTTAA 1440  
OY 1441 TATGTAAAGTGAAGAGTCACTCCAAATCAGTATGAGTAAATATGAAACAAATAT 1500  
| | | | |  
Db 1441 TATGTAAAGTGAAGAGTCACTCCAAATCAGTATGAGTAAATATGAAACAAATAT 1500  
OY 1501 TTGGAAAACTATCGAAGAAAGGCAAGCCTCCCACTTAAGCCATGTAATCAAGAAATC 1560  
| | | | |  
Db 1501 TTGGAAAACTATCGAAGAAAGGCAAGCCTCCCACTTAAGCCATGTAATCAAGAAATC 1560  
OY 1561 TAATTTAGAGCAATTTGTTACTGAGCCACAGATTAATACAGAGCGTCCCTCACAAATA 1620  
| | | | |  
Db 1561 TAATTTAGAGCAATTTGTTACTGAGCCACAGATTAATACAGAGCGTCCCTCACAAATA 1620  
OY 1621 AATTAAGGCTTAAAGAGACCTACATCAGGCTTCAATCCGAGGATTTTATCAAGAAAG 1680  
| | | | |  
Db 1621 AATTAAGGCTTAAAGAGACCTACATCAGGCTTCAATCCGAGGATTTTATCAAGAAAG 1680  
OY 1681 CAGATTTGGCAGTCTCAAAAGACTCCTGAATGATTAATCAGGGAATCAACCAAGCAGAGC 1740  
| | | | |  
Db 1681 CAGATTTGGCAGTCTCAAAAGACTCCTGAATGATTAATCAGGGAATCAACCAAGCAGAGC 1740  
OY 1741 AGAATGCTCAAGTGAATTAATTAATAGTGTGATGAGATTAATAACAAAGGTGATT 1800  
| | | | |  
Db 1741 AGAATGCTCAAGTGAATTAATTAATAGTGTGATGAGATTAATAACAAAGGTGATT 1800  
OY 1801 CTATTCAGATGAGAAAAATCCTAACCAATAGATCATCTGAAAAAAGAAATCTGTTCA 1860  
| | | | |  
Db 1801 CTATTCAGATGAGAAAAATCCTAACCAATAGATCATCTGAAAAAAGAAATCTGTTCA 1860  
OY 1861 AAACGAAAGCTGAACCTATTAAGCAGCACTATTAAGCAATATGGAATCAATTAATATCC 1920  
| | | | |  
Db 1861 AAACGAAAGCTGAACCTATTAAGCAGCACTATTAAGCAATATGGAATCAATTAATATCC 1920  
OY 1921 ACAATTTCAAAAGCACTTAAAGAAATAGCTGAGAGGAGAGTCTTACAGCATATTC 1980  
| | | | |  
Db 1921 ACAATTTCAAAAGCACTTAAAGAAATAGCTGAGAGGAGAGTCTTACAGCATATTC 1980  
OY 1981 ATGCGCTTGAATAGTACTGAGTGAAGTAAATCTAAGCCCACTAATTTGATCAATTTGAAA 2040  
| | | | |  
Db 1981 ATGCGCTTGAATAGTACTGAGTGAAGTAAATCTAAGCCCACTAATTTGATCAATTTGAAA 2040  
OY 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAATATACCAATATGCACTCA 2100  
| | | | |  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAATATACCAATATGCACTCA 2100  
OY 2101 GGCACAGCAAAAGCTTACACTCATGGAAGTAAAGAACTGCAACTGAGCCAAAGAA 2160  
| | | | |  
Db 2101 GGCACAGCAAAAGCTTACACTCATGGAAGTAAAGAACTGCAACTGAGCCAAAGAA 2160  
OY 2161 GTTAAAGCAAAATGAAGCAAGTAAAGACATGACAGGATCACTTCCACAGCTGA 2220  
| | | | |  
Db 2161 GTTAAAGCAAAATGAAGCAAGTAAAGACATGACAGGATCACTTCCACAGCTGA 2220  
OY 2221 AGTTAAACAATGCACTGCTGTTTACTAAGTGTCAAAATACCAAGTGAATTAAGAT 2280  
| | | | |  
Db 2221 AGTTAAACAATGCACTGCTGTTTACTAAGTGTCAAAATACCAAGTGAATTAAGAT 2280  
OY 2281 TTGTCAATCTTAGCTTCCAAAGAGAGAAAAAGAGAAACTAGAAACAGTTAAAGTGT 2340  
| | | | |

Db	2281	TTGTCATCTCAGCTTCCAGAGAAAGAAAAAGAAAGAACTAGAAACGTAAAGTCT	2340
QY	2341	CTAATAATGCTGAAGACCCCAAGAGTCTCATGTTAAGTGAGAAAGGTTTTGCAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGAGTCTCATGTTAAGTGAGAAAGGTTTTGCAACTG	2400
QY	2401	AAAGATCTGTAGAGAGTAGAGATATTTTCATGTGTTACTGTTCTGATTATGGCACTAGG	2460
Db	2401	AAAGATCTGTAGAGAGTAGAGATATTTTCATGTGTTACTGTTCTGATTATGGCACTAGG	2460
QY	2461	AAAGATCTGTTACTGAGAGTTAGACACTGTAGGAAGGCCAAAACAGACCAATAAT	2520
Db	2461	AAAGATCTGTTACTGAGAGTTAGACACTGTAGGAAGGCCAAAACAGACCAATAAT	2520
QY	2521	GTTGAGTCAAGTGTGCAGCATTTTGAAACCCCAAGGAGTAATTCATGTTGTTCCAAAG	2580
Db	2521	GTTGAGTCAAGTGTGCAGCATTTTGAAACCCCAAGGAGTAATTCATGTTGTTCCAAAG	2580
QY	2581	ATAATAGAAAATGACACAGAGGCTTTAAGTATTCATTTGSGACATGAAGTTAAACACAGTC	2640
Db	2581	ATAATAGAAAATGACACAGAGGCTTTAAGTATTCATTTGSGACATGAAGTTAAACACAGTC	2640
QY	2641	GGGAAACAACATATGAAAATGGAAGAAAGTAAGTATATCTCAGTATTTGCGAATATAT	2700
Db	2641	GGGAAACAACATATGAAAATGGAAGAAAGTAAGTATATCTCAGTATTTGCGAATATAT	2700
QY	2701	TCAAGTTTCAAAAGCGGCAGTCAATTTGCTGTTTTCAAATCCAGAAATGCGAGAGAGG	2760
Db	2701	TCAAGTTTCAAAAGCGGCAGTCAATTTGCTGTTTTCAAATCCAGAAATGCGAGAGAGG	2760
QY	2761	AATGTCACACATTTCTGTGCCACTGTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTCACACATTTCTGTGCCACTGTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
QY	2821	TTGGAATGTGAACAAAAGGAAGAAATCAAGAGAAATAGTCTAATATCAAGCTGTAC	2880
Db	2821	TTGGAATGTGAACAAAAGGAAGAAATCAAGAGAAATAGTCTAATATCAAGCTGTAC	2880
QY	2881	AGACAGTAAATATACACTGCGAGGTTTCTGTTGGTGGTCAGAAATATAGCAAGTGTATA	2940
Db	2881	AGACAGTAAATATACACTGCGAGGTTTCTGTTGGTGGTCAGAAATATAGCAAGTGTATA	2940
QY	2941	ATGCCAATGTATGATCTCAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCCAGAGCA	3000
Db	2941	ATGCCAATGTATGATCTCAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCCAGAGCA	3000
QY	3001	ACGAACTGCACTCATTTACTCCAAATTAACATGAGCTTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAACTGCACTCATTTACTCCAAATTAACATGAGCTTTTACAAAACCCATATCGTATAC	3060
QY	3061	CACACATTTTCCCATCAACATCTAATTTGTTAAACTTAATGTAAAGAAAATCTGCTAGAGG	3120
Db	3061	CACACATTTTCCCATCAACATCTAATTTGTTAAACTTAATGTAAAGAAAATCTGCTAGAGG	3120
QY	3121	AAAACTTTGAGGAACATTCATCTCACTCGAAGAAATGGGAATGAGAACTTCCAA	3180
Db	3121	AAAACTTTGAGGAACATTCATCTCACTCGAAGAAATGGGAATGAGAACTTCCAA	3180
QY	3181	GTACAGTGAACCAATTAGCCGTAATTAACATTAGAGAAAATGTTTTTAAGAGCCAGCT	3240
Db	3181	GTACAGTGAACCAATTAGCCGTAATTAACATTAGAGAAAATGTTTTTAAGAGCCAGCT	3240
QY	3241	CAACCAATTAATTAAGAGTGTGTTCCAGATCTAATGAATGGGGCTCCAGTATTAATGAA	3300
Db	3241	CAACCAATTAATTAAGAGTGTGTTCCAGATCTAATGAATGGGGCTCCAGTATTAATGAA	3300
QY	3301	TAGTTCACAGTATGAAGAAACATTCACAGAGAACTAGTATGAACAAGAGGCCCAAAATGGA	3360
Db	3301	TAGTTCACAGTATGAAGAAACATTCACAGAGAACTAGTATGAACAAGAGGCCCAAAATGGA	3360
QY	3361	ATGCTATGCTTAGATTAGGGGTTTGCACCTGAGGCTATTAACAAGTCTTCCGTGGA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTGCACCTGAGGCTATTAACAAGTCTTCCGTGGA	3420

Db	3361	ATGTTATGCTTAAGTTAAGGGGTTTTCGACACCTGAGGTCTATTAACAAAGTCTCTCGTGA	3420
Qy	3421	GTAATTGTAAAGCATCTCTGAATATAAAAAGCAAGATATGAGAGAGTACTGACTGTTA	3480
Db	3421	GTAATTGTAAAGCATCTCTGAATATAAAAAGCAAGATATGAGAGATGTTGACACTGTTA	3480
Qy	3441	ATTAAGATTTCTCTCCATTACTGATTTTCAGATTAACCTTAAGAAGCCTATGGAACTATTC	3540
Db	3481	ATACAGATTTCTCTCCATTACTGATTTTCAGATTAACCTTAAGAAGCCTATGGAACTATTC	3540
Qy	3541	ATGCATCTCAGGGTTGTTCTGAGACACCTGATGACCTGTATGATGATGGTAAATAAAGG	3600
Db	3541	ATGCATCTCAGGGTTGTTCTGAGACACCTGATGACCTGTATGATGATGGTAAATAAAGG	3600
Qy	3601	AAGATACTAGTTTGTGCGAAATGACATTAAGAAAGTCTGCTGTTTTTATAGCAAAACGC	3660
Db	3601	AAGATACTAGTTTGTGCGAAATGACATTAAGAAAGTCTGCTGTTTTTATAGCAAAACGC	3660
Qy	3661	TCCGAAAGAGAGAGCTTACGAGAGATCTAAGCCCTTTCACCCATACACATTTGGCTCAGG	3720
Db	3661	TCCGAAAGAGAGAGCTTACGAGAGATCTAAGCCCTTTCACCCATACACATTTGGCTCAGG	3720
Qy	3721	GTTACCGCAAGGGGGCCCAAAATTTAGAGTCCCTCGAAGAGAACTTATCTAGTGGAGATG	3780
Db	3721	GTTACCGCAAGGGGGCCCAAAATTTAGAGTCCCTCGAAGAGAACTTATCTAGTGGAGATG	3780
Qy	3781	AAGAGCTCCCTGCTTCCACACACTGTATTTGGTAAAGTAACAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTCCCTGCTTCCACACACTGTATTTGGTAAAGTAACAATATACCTTCTCAGT	3840
Qy	3841	CTACTAGGCATAGCACCCGTTGCTACCGAGTGTCTGTAAAGACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCATAGCACCCGTTGCTACCGAGTGTCTGTCTAAAGACACAGAGAGAAATTTAT	3900
Qy	3901	TATCATTTGAAGAAATAGCTTAAATGACTGGAGTAACCAAGGTAATATTGGCAAAAGCATCTC	3960
Db	3901	TATCATTTGAAGAAATAGCTTAAATGACTGGAGTAACCAAGGTAATATTGGCAAAAGCATCTC	3960
Qy	3961	AGGAACATCACTTATAGTGAAGAAACAAATGTCTGCTGATTTGTTTCTTCACAGTCA	4020
Db	3961	AGGAACATCACTTATAGTGAAGAAACAAATGTCTGCTGATTTGTTTCTTCACAGTCA	4020
Qy	4021	GTAATTTGGAAGACTTGACTCTCAATACAAACACCCAGGATCCTTCTTGATTTGGTTCTT	4080
Db	4021	GTAATTTGGAAGACTTGACTCTCAATACAAACACCCAGGATCCTTCTTGATTTGGTTCTT	4080
Qy	4081	CCAAACCAATAGAGGCATCACTCTGAAAGCCAGGAGTTGCTGAGTGACAGAAATTTGG	4140
Db	4081	CCAAACCAATAGAGGCATCACTCTGAAAGCCAGGAGTTGCTGAGTGACAGAAATTTGG	4140
Qy	4141	TTTCAGATGATGAAGAAAGGGAAGGGGCTTGGAAAGAAATATATCAABAAGCAACCA	4200
Db	4141	TTTCAGATGATGAAGAAAGGGAAGGGGCTTGGAAAGAAATATATCAABAAGCAACCA	4200
Qy	4201	TGATTTCAAACTTATAGTGAAGCAAGCATCTGGGGTGTGAAGTGAACCAAGCGCTCTGTAAG	4260
Db	4201	TGATTTCAAACTTATAGTGAAGCAAGCATCTGGGGTGTGAAGTGAACCAAGCGCTCTGTAAG	4260
Qy	4261	ACTGCTCAGGGCTATCCTCTCAAGATGACATTTTAAACCCTCAGCAGAGGAGTACATATGC	4320
Db	4261	ACTGCTCAGGGCTATCCTCTCAAGATGACATTTTAAACCCTCAGCAGAGGAGTACATATGC	4320
Qy	4321	AACATTAACCTGATTAAGCTCCACAGCAAGAAATGGCTGAATTAACCTGTGTGAACACGC	4380
Db	4321	AACATTAACCTGATTAAGCTCCACAGCAAGAAATGGCTGAATTAACCTGTGTGAACACGC	4380
Qy	4381	ATGGAGACCCAGCTTCTTACACAGCTTACCTTCATCATATAGTACTCTTCCCTTGAGG	4440
Db	4381	ATGGAGACCCAGCTTCTTACACAGCTTACCTTCATCATATAGTACTCTTCCCTTGAGG	4440
Qy	4441	ACCTGGCAAAATCCAGAACCAAGCACATCGAAAAAAGACAGATTAATTAACACAGAAAAAGTA	4500
Db	4441	ACCTGGCAAAATCCAGAACCAAGCACATCGAAAAAAGACAGATTAATTAACCTCAAGAAAAAGTA	4500

OY	4501	GTAATACCCATTAAAGCACAATTCACAAGGCCCTTTCGCGACAAGTTGAAGTGTCG	4560
Db	4501	GTCATAACCTATAAGCCAGATATCCABAAGCCCTTTCGTGCACAAAGTTGAAGTGTCG	4560
OY	4561	CAGTAGTCTTACCAGTAAAAAATAAAGAACCCAGAGAGTGGAAAAGGTCAATCCCCTCTAAT	4620
Db	4561	CAGATAGTTCTACAGTAAAAAATAAAGAACCCAGAGAGTGGAAAAGGTCAATCCCCTCTAAT	4620
OY	4621	GCCCCATCATTAAGTAGTAGGTGGACACTGCAACTTCTCTCGGGAGTCCTTAGAATAGAA	4680
Db	4621	GCCCCATCATTAAGTAGTAGGTGGACACTGCAACTTCTCTCGGGAGTCCTTAGAATAGAA	4680
OY	4681	ACTAACCATCTCAAGAGAGAGCTCATTTAAGTTGTGTGATGTGTGAGAGACACAGCTGGAG	4740
Db	4681	ACTAACCATCTCAAGAGAGAGCTCATTTAAGTTGTGTGATGTGTGAGAGACACAGCTGGAG	4740
OY	4741	AGTCTGGGCCACACGATTTTACGGAAAATCTTACTTCCAGGCAAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACACGATTTTACGGAAAATCTTACTTCCAGGCAAGATCTAGAGGAA	4800
OY	4801	CCCCCTACCTGGATCTGGAAATCAGCCTCTCTCTGATGTGACCCGAATCTGATCCTCTG	4860
Db	4801	CCCCCTACCTGGATCTGGAAATCAGCCTCTCTCTGATGTGACCCGAATCTGATCCTCTG	4860
OY	4861	AAGACAGAGCCCCAGAGTCACTGCTGTGTGGCAACATACCATCTTCCAACCTCTCATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCACTGCTGTGTGGCAACATACCATCTTCCAACCTCTCATTTGA	4920
OY	4921	AAGTCCCCCAATTGAAAGTTGCGAANAATCTGCCAGATCCAGAGCTGCTCATCTACTG	4980
Db	4921	AAGTCCCCCAATTGAAAGTTGCGAANAATCTGCCAGATCCAGAGCTGCTCATCTACTG	4980
OY	4981	ATACTGCTGGGTAAATGCAATGGAAGAAGTGTGACAGGAGAGAACCCAGAAATGACAG	5040
Db	4981	ATACTGCTGGGTAAATGCAATGGAAGAAGTGTGACAGGAGAGAACCCAGAAATGACAG	5040
OY	5041	CTTCAACACAAAAGGGTCAACAAAAGAATGTCCATGGTGTCTGCGCCTGACCCAGAG	5100
Db	5041	CTTCAACACAAAAGGGTCAACAAAAGAATGTCCATGGTGTCTGCGCCTGACCCAGAG	5100
OY	5101	AATTTATGCTGCTACGATCAAGTTTGGCGAANAACCCACATCACTTAACTAATTAATTA	5160
Db	5101	AATTTATGCTGCTGATCAAGTTTGGCGAANAACCCACATCACTTAACTAATTAATTA	5160
OY	5161	CTGAAGAGACTACTCATGTTGTATGAAAACAGATGCTGAAGTTGTGTGTAACGAGCAC	5220
Db	5161	CTGAAGAGAGACTACTCATGTTGTATGAAAACAGATGCTGAAGTTGTGTGTAACGAGCAC	5220
OY	5221	TGAATATTTTTCTAGGAATTTGGCGGAGAAAATGGTAGTACTAATTTTGGGTGACC	5280
Db	5221	TGAATATTTTTCTAGGAATTTGGCGGAGAAAATGGTAGTACTAATTTTGGGTGACC	5280
OY	5281	AGCTATTAAAGAAAAGAAAATCTGAATAGCATGATTTTGAAGTACAGAGAGATGTGG	5340
Db	5281	AGCTATTAAAGAAAAGAAAATCTGAATAGCATGATTTTGAAGTACAGAGAGATGTGG	5340
OY	5341	TCAATGGAAGAAACCAACCAAGTCCAAAAGCAGACAGAGAATCCACAGACAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCAACCAAGTCCAAAAGCAGACAGAGAATCCACAGACAGAAAGATCT	5400
OY	5401	TCAGGAGGGCTAGAAATCTGTGTATGTGGGCCCTTCCACCAATATGCCACAGATCACTGG	5460
Db	5401	TCAGGAGGGCTAGAAATCTGTGTATGTGGGCCCTTCCACCAATATGCCACAGATCACTGG	5460
OY	5461	AATGATGCTACAGCTGTGTGCTCTGTCTGTGTGGAAGAGCTTCTCATCTACCTCTG	5520
Db	5461	AATGATGCTACAGCTGTGTGCTCTGTCTGTGTGGAAGAGCTTCTCATCTACCTCTG	5520
OY	5521	GCACAGGTGTCCACCAATTTGTGTGTGTGACAGCCAGATGCTGTGACAGAGACAAATGGCT	5580
Db	5521	GCACAGGTGTCCACCAATTTGTGTGTGTGACAGCCAGATGCTGTGACAGAGACAAATGGCT	5580

QY	5581	TCGAATGCAATTGGGACAGATGAGAGACACCTGTGTGACACCCGAGAGTGGGTGGACA	5640
DB	5581	TCGATGCAATTGGGACAGATGAGAGACACCTGTGTGACACCCGAGAGTGGGTGGACA	5640
QY	5641	GTGTAGCAGCTTACCACTGCGAGAGCTGAGACACCTACTGTATACCCAGATCCGCCACA	5700
DB	5641	GTGTAGCAGCTTACCACTGCGAGAGCTGAGACACCTACTGTATACCCAGATCCGCCACA	5700
QY	5701	GGCACTACTGA 5711	
DB	5701	GGCACTACTGA 5711	
RESULT 12			
ID	T32601	standard; cDNA: 5914 BP.	
AC	T32601;		
DI	19-NOV-1996	(first entry)	
DE	BRCA1, breast and ovarian cancer susceptibility gene.		
KW	BRCA1; breast cancer; ovary cancer; predisposing gene; diagnosis;		
KW	susceptibility gene; prognosis; gene therapy; ds.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	cds	120..5711	
FT		/*tag- a	
FT		/product= BRCA1 protein	
PN	W09605308-A1.		
PD	22-FEB-1996.		
PR	11-AUG-1995; U10220.		
PR	12-AUG-1994; US-289221.		
PR	02-SEP-1994; US-300266.		
PR	16-SEP-1994; US-308104.		
PR	29-NOV-1994; US-348824.		
PR	24-MAR-1995; US-409305.		
PR	07-JUN-1995; US-488011.		
PR	07-JUN-1995; US-483554.		
PR	07-JUN-1995; US-487002.		
PA	(MTRT-) MTRAD GENETICS INC.		
PA	(UTAH) UNIV UTAH RES FOUND.		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
PI	Futreal PA, Goldgar DE, Harsman KD, Kamb A, Miki Y;		
PI	Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV;		
PI	Wiemann RW;		
DR	Wp1: 96-139704/14.		
DR	P-FSDB: R97128.		
PT	New method for diagnosing a predisposition to breast and ovarian		
PT	cancer - by detecting a germline alteration in the BRCA1 gene or		
PT	gene regulatory sequence; for gene therapy and to screen for drugs		
PS	Claim 4; Page 108-117; 200pp: English.		
CC	This is the nucleotide sequence of the breast and ovarian cancer		
CC	susceptibility gene, BRCA1. Four kindred families provided genetic		
CC	evidence for localisation of BRCA1 to a sufficiently small region for		
CC	the application of positional cloning strategies. A detailed map of		
CC	transcripts was developed for the region of 17q21 between D17S1321 and		
CC	D17S1224. A combination of sequences obtd. from cDNA clones,		
CC	hybrid-selected sequences and PCR prods. allowed construction of a		
CC	composite full-length BRCA1 cDNA (see J32612 for genomic sequence).		
CC	The isolated cDNA is used in methods for either diagnosis of the		
CC	predisposition to cancer (partic. breast and ovarian cancer), or for the		
CC	diagnosis or prognosis of cancer, and also in gene-based therapies		
CC	directed at cancer cells.		
SQ	Sequence 5914 BP; 2006 A; 1156 C; 1316 G; 1436 T;		
Query Match 100.0%; Score 5709.4; DB 1; Length 5914;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	AGCTCGCTGAGATTCCTCTGAGCCCGGACAGAGCTGTGGGTTCTCAGATTAACGTGGCC	60
DB	1	AGCTCGCTGAGATTCCTCTGAGCCCGGACAGAGCTGTGGGTTCTCAGATTAACGTGGCC	60
QY	61	CTGTGCTCAGAGACCTTACCTCTGTGCTGGGTAAAGTTCATTGAGACACAAAGAA	120

Db	61	CTGCGCTCAGAGAGCCTTACCCCTCGCTCTGGTAAAGTTCAATGGACAGAAA	120
Qy	121	TGATTTATCTGCTCTTCCGGTTGAAGAAATACAAATGTCTATATGCAAAA	180
Db	121	TGATTTATCTGCTCTTCCGGTTGAAGAAATACAAATGTCTATATGCAAAA	180
Qy	181	TCCTTAGAGTCCCATCTGTCTGGAAGTTGATCAGGAACCTGTCTCCAAAGTACC	240
Db	181	TCCTTAGAGTCCCATCTGTCTGGAAGTTGATCAGGAACCTGTCTCCAAAGTACC	240
Qy	241	ACATATTTTGGAAATTTTGGATGCTGAAATCTCTAACCAAGAAAGAGGCTTCACAGT	300
Db	241	ACATATTTTGGAAATTTTGGATGCTGAAATCTCTAACCAAGAAAGAGGCTTCACAGT	300
Qy	301	GTCCCTTATGTAAAGAAATATTAACCAAAAGAGCCTACAAAGAAAGTACGAGATTATGC	360
Db	301	GTCCCTTATGTAAAGAAATATTAACCAAAAGAGCCTACAAAGAAAGTATGATATTC	360
Qy	361	AACTTGTTGAAGAGCTATTAAATATCTTTGTGCTTTTACGTTGACACAGTTGGAGT	420
Db	361	AACTTGTTGAAGAGCTATTAAATATCTTTGTGCTTTTACGTTTACACAGTTGGAGT	420
Qy	421	ATGCAACAGCTATTAATTTGGCAAAAAAGGAAATATCTCTCTTAACATCTAAAGATG	480
Db	421	ATGCAACAGCTATTAATTTGGCAAAAAAGGAAATATCTCTCTTAACATCTAAAGATG	480
Qy	481	AAAGTTTATCATCAAGATATGGGCTACAGAAACCGTCCCAAAAGACTTCTACAGATG	540
Db	481	AAAGTTTATCATCAAGATATGGGCTACAGAAACCGTCCCAAAAGACTTCTACAGATG	540
Qy	541	AAACCCGAAATCTTCTCTCTGACAGAAACCACTGTCTCACTCTCTAACCTTGGAA	600
Db	541	AAACCCGAAATCTTCTCTCTGACAGAAACCACTGTCTCACTCTCTAACCTTGGAA	600
Qy	601	CTGAGAAACCTCTGAGGACCAAGCAGCGATTAACCTCAAAAGACGTCTGTACATG	660
Db	601	CTGAGAAACCTCTGAGGACCAAGCAGCGGATTAACCTCAAAAGACGTCTGTACATG	660
Qy	661	AATGGGATCGATTCTTCTGAGATTAACCTTAATAGGCAACTATTGACGTGGGAG	720
Db	661	AATGGGATCGATTCTTCTGAGATTAACCTTAATAGGCAACTATTGACGTGGGAG	720
Qy	721	ATCAAGATTTGTTACAATATCACCCTCAAGGAACCAAGGATGAATCAGTTGGATTCTG	780
Db	721	ATCAAGATTTGTTACAATATCACCCTCAAGGAACCAAGGATGAATCAGTTGGATTCTG	780
Qy	781	CAAAAAAGCGCTGTGTGATTTTTTGTGAGACGGATTAACAAATACTGTACATCATAC	840
Db	781	CAAAAAAGCGCTGTGTGATTTTTTGTGAGACGGATTAACAAATACTGTACATCATAC	840
Qy	841	CCAGTAATTAATGATTTTAACACACCTGAGAGGCTGACACTGAGAGGATCCAGAAAGT	900
Db	841	CCAGTAATTAATGATTTTAACACACCTGAGAGGCTGACACTGAGAGGATCCAGAAAGT	900
Qy	901	ATCAGGAGTAGTCTGTTTCAACCTGCATGTGAGGCATGTGGCAAAATACTCATGCCA	960
Db	901	ATCAGGAGTAGTCTGTTTCAACCTGCATGTGAGGCATGTGGCAAAATACTCATGCCA	960
Qy	961	GCTCATTTACAGCATGAGACAGCAGTTTATTCTCACTAAACAGAAATGATGTAGAAA	1020
Db	961	GCTCATTTACAGCATGAGACAGCAGTTTATTCTCACTAAACAGAAATGATGTAGAAA	1020
Qy	1021	AGGCGTAATTTCTGTAAATTAAGCAAAACGCTGGCTTACCAAGAGCCACATTAACAGAT	1080
Db	1021	AGGCGTAATTTCTGTAAATTAAGCAAAACGCTGGCTTACCAAGAGCCACATTAACAGAT	1080
Qy	1081	GGGCTGGAAGTAAGGAACATGTATATGATAGGCGGACTCCAGCACAGAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAGGAACATGTATATGATAGGCGGACTCCAGCACAGAAAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTGTGTGAGAAAAGAAATGAATAGAGAAACTGCCATGCT	1200

Db	1141	ATCGAATGCGTAGCCCTGCTGTGGAGAGAAAGAAATGGAATAGACGAAGAACTGCGATGCT	1200
Qy	1201	CAGAGAAATCCTAGAGATACTGAAGATGTTCTTGATTAACACTAAATAGCAGCATTCAGA	1260
Db	1201	CAGAGAAATCCTAGAGATACTGAAGATGTTCTTGATTAACACTAAATAGCAGCATTCAGA	1260
Qy	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTGAAGTGTAGGTTCTGATGATCACAATGATG	1320
Db	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTGAAGTGTAGGTTCTGATGATCACAATGATG	1320
Qy	1321	GGGAGTCGTAATCAAAATGCCAAAGTAGCTGATGTATGTGACCTTGAATAGGATGATG	1380
Db	1321	GGGAGTCGTAATCAAAATGCCAAAGTAGCTGATGTATGTGACCTTGAATAGGATGATG	1380
Qy	1381	AATATTCGTGTTCTTCAGAGAAATAGACTTACTGCGCCAGTATCCTATGAGGCTTTAA	1440
Db	1381	AATATTCGTGTTCTTCAGAGAAATAGACTTACTGCGCCAGTATCCTATGAGGCTTTAA	1440
Qy	1441	TATGTAAAAGTGAAGAGTTCACATCCAAATCAGTAGAGTAAATTGAAACAAATAT	1500
Db	1441	TATGTAAAAGTGAAGAGTTCACATCCAAATCAGTAGAGTAAATTGAAACAAATAT	1500
Qy	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCCTCCCAACTGAAGCCATGTAACCTGAAATC	1560
Db	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCCTCCCAACTGAAGCCATGTAACCTGAAATC	1560
Qy	1561	TAAATATAGAGCATTTTGTTACTGAGCCACAGATTAATACAGAGCGTCCCTCAAAATA	1620
Db	1561	TAAATATAGAGCATTTTGTTACTGAGCCACAGATTAATACAGAGCGTCCCTCAAAATA	1620
Qy	1621	AATTAAGCCGTAAAAGAGACCTTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG	1680
Db	1621	AATTAAGCCGTAAAAGAGACCTTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAABAACCTCGGAATGTAAATCAGGAACCTAACCAACGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAABAACCTCGGAATGTAAATCAGGAACCTAACCAACGAGC	1740
Qy	1741	AGAATGCTCAAGTATGAATATTACTAATAGTGGTCATGAGTAATAAACAAAAGGTGATT	1800
Db	1741	AGAATGCTCAAGTATGAATATTACTAATAGTGGTCATGAGTAATAAACAAAAGGTGATT	1800
Qy	1801	CTATTCAGAAATGAGAAAAATCCTAACCCATAGAAATCACTCGAAAAAGAAATCTGCTTCA	1860
Db	1801	CTATTCAGAAATGAGAAAAATCCTAACCCATAGAAATCACTCGAAAAAGAAATCTGCTTCA	1860
Qy	1861	AAAGGAAAGCTGAACCTATAAGACAGAGTATAAGCAATGTGAACTCGAAATTAATATCC	1920
Db	1861	AAAGGAAAGCTGAACCTATAAGACAGAGTATAAGCAATGTGAACTCGAAATTAATATCC	1920
Qy	1921	ACAATTCAAAAGACCTTAATAAGATAGGCTGAGAGAGAGTCTTCTACAGGCAATATTC	1980
Db	1921	ACAATTCAAAAGACCTTAATAAGATAGGCTGAGAGAGAGTCTTCTACAGGCAATATTC	1980
Qy	1981	ATGGCTTGAACCTAGTAGTCAGTGAATCTAAGCCCACTAATTGTACTGAATTCGAAA	2040
Db	1981	ATGGCTTGAACCTAGTAGTCAGTGAATCTAAGCCCACTAATTGTACTGAATTCGAAA	2040
Qy	2041	TTGTAGTGTGTTCTAGCAGTAGGAAGAGATTAAGAAAAAAAAGTACACCAAAATGCCAGTCA	2100
Db	2041	TTGTAGTGTGTTCTAGCAGTAGGAAGAGATTAAGAAAAAAAAGTACACCAAAATGCCAGTCA	2100
Qy	2101	GGCAGACAGAAACCTACACATGATGGAAGGTAAAGAACCTGCAACTGAGGCAAGAAAGA	2160
Db	2101	GGCAGACAGAAACCTACACATGATGGAAGGTAAAGAACCTGCAACTGAGGCAAGAAAGA	2160
Qy	2161	GTAACAAGCCAAATGAAACACACATGTAAGAAAGACATGACAGCATCTTCCAGAGCTGA	2220
Db	2161	GTAACAAGCCAAATGAAACACACATGTAAGAAAGACATGACAGCATCTTCCAGAGCTGA	2220
Qy	2221	AGTTAACAAATGACCTGTTCTTTTACTAAGTGTTCAAATACAGTAAGACTTAAGAAAT	2280
Db	2221	AGTTAACAAATGACCTGTTCTTTTACTAAGTGTTCAAATACAGTAAGACTTAAGAAAT	2280



OY	2281	TTTCTCAATCCTTACCCTTCCAAAGAGAGAAAAAAGAAAGAAACCTAGAAACAGTTTAAAGTCT	2340
Db	2281	TTGTCAATCCTTACCCTTCCAAAGAGAGAAAAAAGAAAGAAACCTAGAAACAGTTTAAAGTCT	2340
OY	2341	CTATATATGCTGGAAGACCCCAAGATGCTCATGTGTAAATGGAGAAAGGGTTTGGCAACTG	2400
Db	2341	CTATATATGCTGGAAGACCCCAAGATGCTCATGTGTAAATGGAGAAAGGGTTTGGCAACTG	2400
OY	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCATTTGGTAACTGGTACTGATTTATGGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCATTTGGTAACTGGTAACTGATTTATGGCACTCAGG	2460
OY	2461	AAAGTATCTGCTACTGGAAGTAGCAGCTGTAGGGAAGGCAAAAACGAACCAATTAAT	2520
Db	2461	AAAGTATCTGCTACTGGAAGTAGCAGCTGTAGGGAAGGCAAAAACGAACCAATTAAT	2520
OY	2521	GTGTGAGTCAGTGTGCAGCATTTTGAAAAACCCCAAGGAGCTAATTTCATGGTTGTTCCAAG	2580
Db	2521	GTGTGAGTCAGTGTGCAGCATTTTGAAAAACCCCAAGGAGCTAATTTCATGGTTGTTCCAAG	2580
OY	2581	ATATATGAAATGACACAGAAAGGCTTTAAATATCATTTGGGACATGAAGTTTAAACCACAGTC	2640
Db	2581	ATATATGAAATGACACAGAAAGGCTTTAAATATCATTTGGGACATGAAGTTTAAACCACAGTC	2640
OY	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTAACTGATGCTCAGTATTTGACAGATACAT	2700
Db	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTAACTGATGCTCAGTATTTGACAGATACAT	2700
OY	2701	TCAGGTTTCAAAGGCCCACTATTGCTCTGTTTTCAAATCCAGAGAAATGACAGAAAGG	2760
Db	2701	TCAGGTTTCAAAGGCCCACTATTGCTCTGTTTTCAAATCCAGAGAAATGACAGAAAGG	2760
OY	2761	AATGTCAACATCTCTGCCCCACTGCGGGGCTTAAAGAAACAAAGTCCAAAGTACACTT	2820
Db	2761	AATGTCAACATCTCTGCCCCACTGCGGGGCTTAAAGAAACAAAGTCCAAAGTACACTT	2820
OY	2821	TTTGAATGTGAACAAAAGGAAAGAAATCAAGGAAAGATGAGTAAATATCAAGCTGTAC	2880
Db	2821	TTTGAATGTGAACAAAAGGAAAGAAATCAAGGAAAGATGAGTAAATATCAAGCTGTAC	2880
OY	2881	AACAGGTTAATATCACTGCGAGGCTTTCCTGTGGTGTGTCGAAAAGATTAAGCCAGTTGATA	2940
Db	2881	AACAGGTTAATATCACTGCGAGGCTTTCCTGTGGTGTGTCGAAAAGATTAAGCCAGTTGATA	2940
OY	2941	ATGCCAAATGTAGTATCAAGAGAGGCTCATGTGTTTGTCTATCATCTCAGTTCAAGAGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAGAGAGGCTCATGTGTTTGTCTATCATCTCAGTTCAAGAGCA	3000
OY	3001	ACGAAACTGGACTCATTACTCCAAATTAACATGTGACTTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAAACTGGACTCATTACTCCAAATTAACATGTGACTTTTACAAAACCCATATCGTATAC	3060
OY	3061	CACCACTTTTCCCATCAAGTCAATTGTGTAAACTTAATGTAGAAGAAAATCTGTGAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCAATTGTGTGTAAACTTAATGTAGAAGAAAATCTGTGAGG	3120
OY	3121	AAAACCTTGTAGGACATTTCAATGTCACTGTGAAGAGAAAATGSGAAAATGAGACATTTCCA	3180
Db	3121	AAAACCTTGTAGGACATTTCAATGTCACTGTGAAGAGAAAATGSGAAAATGAGACATTTCCA	3180
OY	3181	GTACAGTGTGACAAATTTACCCGTAATTAACATTGAGAAAAATGTTTTTAAAGAACCAAGCT	3240
Db	3181	GTACAGTGTGACAAATTTACCCGTAATTAACATTGAGAAAAATGTTTTTAAAGAACCAAGCT	3240
OY	3241	CAAGCAATTTTATGAAGTAGGTTCCAGTACTAATGAAGGGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATTTTATGAAGTAGGTTCCAGTACTAATGAAGGGGCTCCAGTATTAATGAAA	3300
OY	3301	TAGGTTCCAGTATGAAGAAATTTCAAGCAGAACTAGGTAGAAAACAGGGCCAAAATTGA	3360
Db	3301	TAGGTTCCAGTATGAAGAAATTTCAAGCAGAACTAGGTAGAAAACAGGGCCAAAATTGA	3360

OY	3361	ATGCTATGCTTAAGTTAGGGGTTTGTGCAACCTGAGGCTATATAAACAAAGTCTCTCGGAA	3420
Db	3361	ATGCTATGCTTAAGTTAGGGGTTTGTGCAACCTGAGGCTATATAAACAAAGTCTCTCGGAA	3420
OY	3421	GTAATGTAAAGCATCCGAAATATAAAAACCAAGATATGAAGAGTAGTACAGACTGTAA	3480
Db	3421	GTAATGTAAAGCATCCGAAATATAAAAACCAAGATATGAAGAGTAGTACAGACTGTAA	3480
OY	3481	ATACAGATTTCTCCTCATATCTGATTTTACAGATTAAGTAAACAGCCTATGGGAAGTAGTC	3540
Db	3481	ATACAGATTTCTCCTCATATCTGATTTTACAGATTAAGTAAACAGCCTATGGGAAGTAGTC	3540
OY	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTTATGATGATGTGAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTTATGATGATGTGAATTAAGG	3600
OY	3601	AAGATACAGTTTGGCGAAAAATGACATTAAGGAAAGTTCGCTGTTTATGCAAAAAGG	3660
Db	3601	AAGATACAGTTTGGCGAAAAATGACATTAAGGAAAGTTCGCTGTTTATGCAAAAAGG	3660
OY	3661	TCCAGAAAGGAGAGCTTAGCAGAGAGTCTTAGGCCCTTCCACCATACATATTTGGCTCAGG	3720
Db	3661	TCCAGAAAGGAGAGCTTAGCAGAGAGTCTTAGGCCCTTCCACCATACATATTTGGCTCAGG	3720
OY	3721	GTTACCCGAAGAGGGCCAAAGAAATTAAGTCTCTCAAGAGAGACTTATCTAGTGAGATG	3780
Db	3721	GTTACCCGAAGAGGGGGCCAAAGAAATTAAGTCTCTCAAGAGAGAACTTATCTAGTGAGAGATG	3780
OY	3781	AAGAGCTCCCTCGTCCAAACCTGTATATTTGGTAAAGTAACAAATATCCCTTCACAT	3840
Db	3781	AAGAGCTCCCTCGTCCAAACCTGTATATTTGGTAAAGTAACAAATATCCCTTCACAT	3840
OY	3841	CTATAGGAGCATACACCGTTGTCTACCGAGTGTCTGTCTGAAGACACAGAGAGAAATTTAT	3900
Db	3841	CTATAGGAGCATACACCGTTGTCTACCGAGTGTCTGTCTGAAGACACAGAGAGAAATTTAT	3900
OY	3901	TATCATTTGAAGAAATAGCTTTAAATGACTGCAGTAACCAAGTAAATTTGGCCAAAGGCACTTC	3960
Db	3901	TATCATTTGAAGAAATAGCTTTAAATGACTGCAGTAACCAAGTAAATTTGGCCAAAGGCACTTC	3960
OY	3961	AGGAACATCACTTAATGAGGAAACAAAATGTCTGCTAGCTTGTCTTCTCACAGTGA	4020
Db	3961	AGGAACATCACTTAATGAGGAAACAAAATGTCTGCTAGCTTGTCTTCTCACAGTGA	4020
OY	4021	GTTGAATTTGGAAGACTTGACATGCGAAATACAAACACCCAGAGACTCTTCTTGATTTGGTCT	4080
Db	4021	GTTGAATTTGGAAGACTTGACATGCGAAATACAAACACCCAGAGACTCTTCTTGATTTGGTCT	4080
OY	4081	CCAAACAAATGAGGCAATCAGTGTGAAAGCCAGGAGATTGTCTGAGTGAACAAGAAATTGG	4140
Db	4081	CCAAACAAATGAGGCAATCAGTGTGAAAGCCAGGAGATTGTCTGAGTGAACAAGAAATTGG	4140
OY	4141	TTTTCAGATGATGAAAGAAAGAGAAAGGGCTTGGAAAGAAATATCAAGAGAGGCAAAAGCA	4200
Db	4141	TTTTCAGATGATGAAAGAAAGAGAAAGGGCTTGGAAAGAAATATCAAGAGAGGCAAAAGCA	4200
OY	4201	TGATTTCAAACTTAGGTGAAGAGAGCATTTGGGTTGTGAGAGTGAAGAAACAAGGCTCTGAAAG	4260
Db	4201	TGATTTCAAACTTAGGTGAAGAGAGCATTTGGGTTGTGAGAGTGAAGAAACAAGGCTCTGAAAG	4260
OY	4261	ACTGCTCAGGGCTATCTCTCAGATGAGCATTTTAACTCAGCAGAGAGGATATCCATGTC	4320
Db	4261	ACTGCTCAGGGCTATCTCTCAGATGAGCATTTTAACTCAGCAGAGAGGATATCCATGTC	4320
OY	4321	AACATTAACCTGATTAAGCTTCCACGACGAGAAATGCTGTAACCTAGAAAGCTGTGTTAGAACAGC	4380
Db	4321	AACATTAACCTGATTAAGCTTCCACGACGAGAAATGCTGTAACCTAGAAAGCTGTGTTAGAACAGC	4380
OY	4381	ATGGAGGCCAGCCTTCTTAACACTACCTTCCATCAATTAAGTACTCTTCTGCGCTTTGAGG	4440
Db	4381	ATGGAGGCCAGCCTTCTTAACACTACCTTCCATCAATTAAGTACTCTTCTGCGCTTTGAGG	4440
OY	4441	ACCTGGGAATCCGAGAACCAAGCATATGAGAAAGAGAGATTAATCTTACAGAAAGATGA	4500



```

Db 4441 ACCGGAATCCAGACAAAGACATCAGAAAAAGCAGTATTAATTCAGAAAAAGTA 4500
Qy 4501 GTGAATACCCATATAGCCAGAAATCCAGAGGCCCTTCTGCTGCAAGTTTGAGTGTCTG 4560
Db 4501 GTGAATACCCATATAGCCAGAAATCCAGAGGCCCTTCTGCTGCAAGTTTGAGTGTCTG 4560
Qy 4561 CAGATAGTTCTTACAGTAAAAAATAAAGAACAGAGAGTGGAAAGGTATCCCTTCTTAAT 4620
Db 4561 CAGATAGTTCTTACAGTAAAAAATAAAGAACAGAGAGTGGAAAGGTATCCCTTCTTAAT 4620
Qy 4621 GCCCATCATATAGTATGATGTGTATGATGATGATGATGATGATGATGATGATGATGAT 4680
Db 4621 GCCCATCATATAGTATGATGTGTATGATGATGATGATGATGATGATGATGATGATGAT 4680
Qy 4681 ACTACCATCTCTAAGAGAGAGCTCATTAAGTGTGTATGATGATGATGATGATGATGATGAT 4740
Db 4681 ACTACCATCTCTAAGAGAGAGCTCATTAAGTGTGTATGATGATGATGATGATGATGATGAT 4740
Qy 4741 AGTCTGGCCACACGATTTTGAGGAAAAATCTTACTTGGCAAGCAAGATCTAGAGGAA 4800
Db 4741 AGTCTGGCCACACGATTTTGAGGAAAAATCTTACTTGGCAAGCAAGATCTAGAGGAA 4800
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTCTCTGATGATACCTGAAATCTGATCTCTG 4860
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTCTCTGATGATACCTGAAATCTGATCTCTG 4860
Qy 4861 AAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4920
Db 4861 AAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4920
Qy 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTGCTCATACTACTG 4980
Db 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTGCTCATACTACTG 4980
Qy 4981 ATACCTCTGGGTATATGAAATGGAAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040
Db 4981 ATACCTCTGGGTATATGAAATGGAAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040
Qy 5041 CTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5100
Db 5041 CTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5100
Qy 5101 AATTTATGCTCGTGTACAAAGTTGCCAGAAAAACACCAATCACTTAATTAATTA 5160
Db 5101 AATTTATGCTCGTGTACAAAGTTGCCAGAAAAACACCAATCACTTAATTAATTA 5160
Qy 5161 CTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5220
Db 5161 CTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5220
Qy 5221 TGAATATATTTTGTAGGAATTTGGGAGAGAAATGGTATGATGATGATGATGATGATGATG 5280
Db 5221 TGAATATATTTTGTAGGAATTTGGGAGAGAAATGGTATGATGATGATGATGATGATGATG 5280
Qy 5281 AGCTATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5340
Db 5281 AGCTATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5340
Qy 5341 TGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5400
Db 5341 TGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5400
Qy 5401 TCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5460
Db 5401 TCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5460
Qy 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
Db 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
Qy 5521 GCACAGGTGCCCAATTTGTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5580

```

```

Db 5521 GCACAGGTGCCCAATTTGTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5580
Qy 5581 TCCATGCAATTTGGGAGAGATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5640
Db 5581 TCCATGCAATTTGGGAGAGATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5640
Qy 5641 GTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
Db 5641 GTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 13
ID T84840 standard; cDNA to mRNA; 5712 BP.
AC T84840; 21-FEB-1998 (first entry)
DE Human breast and ovarian cancer susceptibility gene BRCA1.
KW BRCA1; breast cancer; ovarian cancer; human;
KW tumour suppressor gene; gene therapy; receptor; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 120..5711
FT /tag= a
FT /transl_except= (pos:1482..1484, aa:Asp)
FT /transl_except= (pos:1581..1583, aa:Ser)
FT /transl_except= (pos:1889..1901, aa:Glu)
FT /transl_except= (pos:1902..1904, aa:Leu)
FT /transl_except= (pos:1905..1907, aa:Glu)
FT /transl_except= (pos:1908..1910, aa:Leu)
FT /transl_except= (pos:1911..1913, aa:Asn)
FT /transl_except= (pos:1914..1916, aa:Asn)
FT /transl_except= (pos:1917..1919, aa:Met)
FT /transl_except= (pos:4476..4478, aa:Val)
FT /transl_except= (pos:4476..4478, aa:Val)
FT /transl_except= (pos:4479..4481, aa:Leu)
FT /transl_except= (pos:4482..4484, aa:Gln)
FT /transl_except= (pos:4689..4691, aa:Pro)

MO9730108-A1.
PD 21-AUG-1997.
PF 19-FEB-1997; U03340.
PR 20-FEB-1996; U5-603753.
PA (UYVA-) UNIV VANDERBILT.
PA (UNIM) UNIV WASHINGTON.
PI Claire-King M, Holt JT, Jensen RA, Jetton TL, Page DL,
PI Robinson-Benion CL, Szabo CI, Thompson ME;
DR P-PSDB; W23286.
DR BRCA1 and BRCA2 tumour suppressor gene products - useful to inhibit
PT breast and ovarian cancer cell growth and tumorigenesis, or treat
PT gene linked hereditary or sporadic ovarian or breast cancer
PS Clam 13; Page 54-63; 148bp; English.
CC This sequence comprises a full-length BRCA1 cDNA. Genetic analysis
CC of familial and ovarian cancer indicates that BRCA1 is a tumour
CC suppressor gene. It encodes a 190 kDa protein (see W23286) that is
CC an inhibitor of the growth and proliferation of human breast and
CC ovarian cancer cells. DNA encoding the BRCA1 protein can thus be
CC used in gene therapy methods for the treatment of breast and
CC ovarian cancers. A purified BRCA1 protein can also be used to treat
CC these cancers and, since it is secreted, can be used to identify
CC the BRCA1 receptor and hence to identify BRCA1 protein-mimetic
CC agents which act on the receptor for use in breast and ovarian
CC cancer treatment. The BRCA2 gene (see T84411) and BRCA2 protein
CC (see W23287) have also been characterised. Methods are claimed for
CC the isolation of BRCA1 or BRCA2 receptors, and for treating or
CC preventing breast and (gene-linked hereditary or sporadic) ovarian
CC cancers using BRCA1 and BRCA2 proteins and genes.
SC Sequence 5712 BP; 1956 A; 1099 C; 1274 G; 1383 T;

```

Query Match		100.0%;	Score 5709.4;	DB 1;	Length 5712;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 5710; Conservative		0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1 AGCTGCTGAGACTTCTCTGAGACCCCGACACGCTGTGGGTTTCAGATACTGGGCC 60				
DB	1 AGCTGCTGAGACTTCTCTGAGACCCCGACACGCTGTGGGTTTCAGATACTGGGCC 60				
QY	61 CCTGCGCTCAGAGAGCCCTTCACCCCTGCTGTGGGTAAAGTTCATTGGAACAGAAAATA 120				
DB	61 CCTGCGCTCAGAGAGCCCTTCACCCCTGCTGTGGGTAAAGTTCATTGGAACAGAAAATA 120				
QY	121 TGGATTATCTGCTCTTCCGCTTGAGAAAGTACAAATGTCATTATGCTATCAGAAAA 180				
DB	121 TGGATTATCTGCTCTTCCGCTTGAGAAAGTACAAATGTCATTATGCTATCAGAAAA 180				
QY	181 TCTTAGAGTGTCCACTCTCTGAGAGTTGATCAGAGAACCTGTCTCCACAAAGTGTACC 240				
DB	181 TCTTAGAGTGTCCACTCTCTGAGAGTTGATCAGAGAACCTGTCTCCACAAAGTGTACC 240				
QY	241 ACATATTTTGCATAATTTTGCAATGCTGTAACCTCTCAACAGAAAGAAAGGCTTCACAGT 300				
DB	241 ACATATTTTGCATAATTTTGCAATGCTGTAACCTCTCAACAGAAAGAAAGGCTTCACAGT 300				
QY	301 GTCCTTTATGTAGATGATATACCAAAAGAGCCTACAGAAAGTACAGATTTAGTC 360				
DB	301 GTCCTTTATGTAGATGATATACCAAAAGAGCCTACAGAAAGTACAGATTTAGTC 360				
QY	361 AACTGTGTGAAGAGCTATTTGAAATCATTTTGCTTTTCAGCTTGACAGAGTTGGAGT 420				
DB	361 AACTGTGTGAAGAGCTATTTGAAATCATTTTGCTTTTCAGCTTGACAGAGTTGGAGT 420				
QY	421 ATGCAAAAGCTATATTTTGCAAAAAAGAAATATACCTCTCTGAACATCTAAAAGATG 480				
DB	421 ATGCAAAAGCTATATATTTTGCAAAAAAGAAATATACCTCTCTGAACATCTAAAAGATG 480				
QY	481 AAGTTTCTATCTCCAAAGTATGGGTACAGAAACCGTCCCAAAAGACTTCTACAGAGTG 540				
DB	481 AAGTTTCTATCTCCAAAGTATGGGTACAGAAACCGTCCCAAAAGACTTCTACAGAGTG 540				
QY	541 AACCCGAAATCTCTCTGAGAAACCAAGTCTCAGTGTCCAACTCTTAACTTTGAA 600				
DB	541 AACCCGAAATCTCTCTGAGAAACCAAGTCTCAGTGTCCAACTCTTAACTTTGAA 600				
QY	601 CTGTGAGAACTCTGAGCAAAAGCAGCGATACAACTCTCAAAAGAGCTGTCTCATATG 660				
DB	601 CTGTGAGAACTCTGAGCAAAAGCAGCGATACAACTCTCAAAAGAGCTGTCTCATATG 660				
QY	661 AATTGGATCTGATCTCTGAAAGATACCGTTAATAAAGCACTTATGCAAGTGGGAG 720				
DB	661 AATTGGATCTGATCTCTGAAAGATACCGTTAATAAAGCACTTATGCAAGTGGGAG 720				
QY	721 ATCAAGAAATGTGTACAAATACACCCCTCAAGAAACAGGATGAATCAATTTGATTCG 780				
DB	721 ATCAAGAAATGTGTACAAATACACCCCTCAAGAAACAGGATGAATCAATTTGATTCG 780				
QY	781 CAAAAAGGCTGCTGTGTAATTTCTGAGACGATGTAACTGTAACATCTCATCAAC 840				
DB	781 CAAAAAGGCTGCTGTGTAATTTCTGAGACGATGTAACTGTAACATCTGTAACATCAAC 840				
QY	841 CCATTAATATGATTTGAAACACCACTGAGAACGCTGACAGCTAGAGGCAATCCAGAAAGT 900				
DB	841 CCATTAATATGATTTGAAACACCACTGAGAACGCTGACAGCTAGAGGCAATCCAGAAAGT 900				
QY	901 ATCAGGAGTGTCTGTTTCAAACTTGATGTGAGACCATGTGGCAAAATATCATGTGCA 960				
DB	901 ATCAGGAGTGTCTGTTTCAAACTTGATGTGAGACCATGTGGCAAAATATCATGTGCA 960				
QY	961 GCTTATTACAGACAGAGAAACAGCACTTTATCTACTTAAGACAGAAATGATGTAGAAA 1020				
DB	961 GCTTATTACAGACAGAGAAACAGCACTTTATCTACTTAAGACAGAAATGATGTAGAAA 1020				
QY	1021 AGGCTGAATCTGTATATATAAGCAAAAGCGCTTGAGCAAGGAGCCAACTAATACAGAT 1080				
DB	1021 AGGCTGAATCTGTATATATAAGCAAAAGCGCTTGAGCAAGGAGCCAACTAATACAGAT 1080				
QY	1081 GGGCTGGAAGTAAAGAAACATGATGATAGCGGACCTCCAGACAGAAAAAAGGTAG 1140				
DB	1081 GGGCTGGAAGTAAAGAAACATGATGATAGCGGACCTCCAGACAGAAAAAAGGTAG 1140				
QY	1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAAAGTGAATTAAGCAGAACTGCCATGCT 1200				
DB	1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAAAGTGAATTAAGCAGAACTGCCATGCT 1200				
QY	1201 CAGAGAACTCTGAGATCTGAGATGTTCCCTGATTAACCTAAATAGCAGCTTACAG 1260				
DB	1201 CAGAGAACTCTGAGATCTGAGATGTTCCCTGATTAACCTAAATAGCAGCTTACAG 1260				
QY	1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATGTAAGTGTGTTGATGATGACATGATG 1320				
DB	1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATGTAAGTGTGTTGATGATGACATGATG 1320				
QY	1321 GGGAGCTGTGAATCAAAATGCAAAAGTGTGATGTATGAGAGCTTCTAAATGAGTAGATG 1380				
DB	1321 GGGAGCTGTGAATCAAAATGCAAAAGTGTGATGTATGAGAGCTTCTAAATGAGTAGATG 1380				
QY	1381 AATATTCGCTCTTCCAGAGAAATAAGACTAGTCCAGTGAATCCATGAGGCTTTAA 1440				
DB	1381 AATATTCGCTCTTCCAGAGAAATAAGACTAGTCCAGTGAATCCATGAGGCTTTAA 1440				
QY	1441 TATGTAAAGTGAAGATTCATCTCAATCAGTAGAGATGATATGAAAGCAAAATAT 1500				
DB	1441 TATGTAAAGTGAAGATTCATCTCAATCAGTAGAGATGATATGAAAGCAAAATAT 1500				
QY	1501 TTGGGAAAACCTATGTGGAAGAAAGGCAAGCTCCCACTTAAGCATGTATGAAAATC 1560				
DB	1501 TTGGGAAAACCTATGTGGAAGAAAGGCAAGCTCCCACTTAAGCATGTATGAAAATC 1560				
QY	1561 TATATATGAGCAATTTTCTACTGAGCAAGATATACAAAGAGCGCCCTCAGAAATA 1620				
DB	1561 TATATATGAGCAATTTTCTACTGAGCAAGATATACAAAGAGCGCCCTCAGAAATA 1620				
QY	1621 AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCACTCTGAGAGATTTTATCAAGAAAG 1680				
DB	1621 AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCACTCTGAGAGATTTTATCAAGAAAG 1680				
QY	1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAAGGAACTTAACCAACGAGC 1740				
DB	1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAAGGAACTTAACCAACGAGC 1740				
QY	1741 AGAATGTCAGTGAATTTTCTAATAGTGTGCTATGAGAAATTAACAAAGAGTGAT 1800				
DB	1741 AGAATGTCAGTGAATTTTCTAATAGTGTGCTATGAGAAATTAACAAAGAGTGAT 1800				
QY	1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGATCTGCTTCA 1860				
DB	1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGATCTGCTTCA 1860				
QY	1861 AAAGCAAAAGCTGAACTTAAGCAGCAGTATAGCAATATGGAATCTGAAATTAATATCC 1920				
DB	1861 AAAGCAAAAGCTGAACTTAAGCAGCAGTATAGCAATATGGAATCTGAAATTAATATCC 1920				
QY	1921 ACAATTCAAAAGCACTTAAGAAAGATAGGCTGAGAGAGAGTCTTACACAGGCAATATC 1980				
DB	1921 ACAATTCAAAAGCACTTAAGAAAGATAGGCTGAGAGAGAGTCTTACACAGGCAATATC 1980				
QY	1981 ATGGCTTGAACCTAGTAGTCAAGAAATTAAGCCCACTTAATTTGATGATGATTCGAAA 2040				
DB	1981 ATGGCTTGAACCTAGTAGTCAAGAAATTAAGCCCACTTAATTTGATGATGATTCGAAA 2040				
QY	2041 TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAAAAGTCAACCAAAATGCCAGTCA 2100				
DB	2041 TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAAAAGTCAACCAAAATGCCAGTCA 2100				
QY	2101 GGCACAGAAAGCTCAACTCATGTGAAGGTAAAGAACTGCACTGAGAGCCAAAGAA 2160				
DB	2101 GGCACAGAAAGCTCAACTCATGTGAAGGTAAAGAACTGCACTGAGAGCCAAAGAA 2160				



QY 4321 AACATACCTGATTAAGCTCCAGAGAAATGGCTGAAGTGTGTAGAACAC 4380  
 |||||  
 Db 4321 AACATACCTGATTAAGCTCCAGAGAAATGGCTGAAGTGTGTAGAACAC 4380  
 QY 4381 ATGGAGCCAGCTTCTACAGCTACCTCCATCAATAGGACTCTTCCCTTGAGG 4440  
 |||||  
 Db 4381 ATGGAGCCAGCTTCTACAGCTACCTCCATCAATAGGACTCTTCCCTTGAGG 4440  
 QY 4441 ACCTGGAAATCCAGAACACATCAGAAAAAGCAGTATTACTTCACAGAAAGTA 4500  
 |||||  
 Db 4441 ACCTGGAAATCCAGAACACATCAGAAAAAGCAGTATTACTTCACAGAAAGTA 4500  
 QY 4501 GTGAATACCTTATAGCCAAATCCAGAAAGCCCTTCTGCTGANAATTTGAGGTGCTG 4560  
 |||||  
 Db 4501 GTGAATACCTTATAGCCAAATCCAGAAAGCCCTTCTGCTGANAATTTGAGGTGCTG 4560  
 QY 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
 |||||  
 Db 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
 QY 4621 GCCCATCATTAAGTATAGTGTGATGACATGACAGTGTCTGGAGTCTTCAGAAATGAA 4680  
 |||||  
 Db 4621 GCCCATCATTAAGTATAGTGTGATGACATGACAGTGTCTGGAGTCTTCAGAAATGAA 4680  
 QY 4681 ACTACCATCTCAAGAGAGCTCATTAAGTGTGTGATGATGAGAGACACAGCTGGAAG 4740  
 |||||  
 Db 4681 ACTACCATCTCAAGAGAGCTCATTAAGTGTGTGATGATGAGAGACACAGCTGGAAG 4740  
 QY 4741 AGTCTGGCCACACAGATTTGACGAAACATCTTACTGCCAAGCAGATCTAGAGGAA 4800  
 |||||  
 Db 4741 AGTCTGGCCACACAGATTTGACGAAACATCTTACTGCCAAGCAGATCTAGAGGAA 4800  
 QY 4801 CCCCTTACCTGCAATCTGCAATCAGCTCTTCTGTGATGACCTGAAATCTGATCTCTG 4860  
 |||||  
 Db 4801 CCCCTTACCTGCAATCTGCAATCAGCTCTTCTGTGATGACCTGAAATCTGATCTCTG 4860  
 QY 4861 AAGACAGAGCCAGAGTACGTCTGTGGCAACATCTTCAACCTCTGCAATGTA 4920  
 |||||  
 Db 4861 AAGACAGAGCCAGAGTACGTCTGTGGCAACATCTTCAACCTCTGCAATGTA 4920  
 QY 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGTGTCTCATACTACTG 4980  
 |||||  
 Db 4921 AAGTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGTGTCTCATACTACTG 4980  
 QY 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGACAGGAGAACCCAGAAATGACAG 5040  
 |||||  
 Db 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGACAGGAGAACCCAGAAATGACAG 5040  
 QY 5041 CTTCAACAGAAAGGTCACAAAGAAATGCAATGCTGTGGCTGACCCAGAGAG 5100  
 |||||  
 Db 5041 CTTCAACAGAAAGGTCACAAAGAAATGCAATGCTGTGGCTGACCCAGAGAG 5100  
 QY 5101 AATTTATGCTGTGACAAAGTTTGCAGAAACACCAATCACTTAACTAATTA 5160  
 |||||  
 Db 5101 AATTTATGCTGTGACAAAGTTTGCAGAAACACCAATCACTTAACTAATTA 5160  
 QY 5161 CTGAAGAGACTCTCTATGTTGTTATGAAACAGATCTGAGTTGTGTGAAAGGACAC 5220  
 |||||  
 Db 5161 CTGAAGAGACTCTCTATGTTGTTATGAAACAGATCTGAGTTGTGTGAAAGGACAC 5220  
 QY 5221 TGAATATTTTGTAGAAATGGGGAGAAATGGGTAGTACTTATTTCTGGGTGACCC 5280  
 |||||  
 Db 5221 TGAATATTTTGTAGAAATGGGGAGAAATGGGTAGTACTTATTTCTGGGTGACCC 5280  
 QY 5281 AGTCTATTAAAGAAATGCTGATATGAGCATATTTTGAAGTCAGAGGAGATGTG 5340  
 |||||  
 Db 5281 AGTCTATTAAAGAAATGCTGATATGAGCATATTTTGAAGTCAGAGGAGATGTG 5340  
 QY 5341 TCAATGGAAGAAACCAAGGTCACAAAGGTCAGAGCAAGAGATCCAGAGCAAGAAATCT 5400  
 |||||  
 Db 5341 TCAATGGAAGAAACCAAGGTCACAAAGGTCAGAGCAAGAGATCCAGAGCAAGAAATCT 5400  
 QY 5401 TCAGGGGGCTAATAATCTTGTGTATGGGCCCTTCAACAAATGCCACAGATCAACTG 5460

Db 5401 TCAGGGGGCTAATAATCTTGTGTATGGGCCCTTCAACAAATGCCACAGATCAACTG 5460  
 |||||  
 QY 5461 AATGATGATGACAGCTGTGTGCTTCTGTGTGTAAGAGCTTTCATATCACCTTG 5520  
 |||||  
 Db 5461 AATGATGATGACAGCTGTGTGCTTCTGTGTGTAAGAGCTTTCATATCACCTTG 5520  
 QY 5521 GCACAGGTGTCCACCAATTTGTTGTGACAGCAGATCTCTGAGACAGAGCAATGGCT 5580  
 |||||  
 Db 5521 GCACAGGTGTCCACCAATTTGTTGTGACAGCAGATCTCTGAGACAGAGCAATGGCT 5580  
 QY 5581 TCCATGCAATTTGGCAGATGTGAGCACCTGTGTGACCCAGAGTGGTGGACA 5640  
 |||||  
 Db 5581 TCCATGCAATTTGGCAGATGTGAGCACCTGTGTGACCCAGAGTGGTGGACA 5640  
 QY 5641 GTGTAGCAGCTCTACAGTGCAGAGCTGGACACTACTGATATACCCAGATCCCCACA 5700  
 |||||  
 Db 5641 GTGTAGCAGCTCTACAGTGCAGAGCTGGACACTACTGATATACCCAGATCCCCACA 5700  
 QY 5701 GCCACTACTGA 5711  
 |||||  
 Db 5701 GCCACTACTGA 5711

## RESULT 14

ID T18311 standard; cDNA; 5914 BP.  
 AC T18311;  
 DT 05-JUN-1996 (first entry)  
 DE BRCA1 gene nonsense allele.  
 KW BRCA1; breast cancer; ovary cancer; predisposing gene;  
 OS Homo sapiens.  
 FH key Location/Qualifiers  
 FT cds 120..4058  
 FT /tag= a  
 FT /tag= b  
 FT /note= "wild-type BRCA1 has C at position 4056"  
 PN W09605307-A2.  
 PD 22-FEB-1996.  
 PF 11-AUG-1995; U10203.  
 PR 12-AUG-1994; US-289221.  
 PR 02-SEP-1994; US-300266.  
 PR 16-SEP-1994; US-308104.  
 PR 29-NOV-1994; US-348824.  
 PR 24-MAR-1995; US-409305.  
 PR 07-JUN-1995; US-488011.  
 PR 07-JUN-1995; US-483554.  
 PR 07-JUN-1995; US-487002.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PA (UTAH) UNIV UTAH RES FOUND.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 PI Futrel AP, Goldgar DE, Harsman KD, Kamb A, Miki Y,  
 PI Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV,  
 PI Wiseman RW;  
 DR WPI; 96-139703/14.  
 PT New isolated human cancer predisposing gene, BRCA1 - used to develop  
 PT prods. for diagnosis, prognosis and therapy of cancers, partic.  
 PT breast and ovarian cancers  
 PS Claim 9, Page 108-117; 190pp; English.  
 CC A BRCA1 susceptibility allele (T18311) was detected in a kindred  
 CC having a nearly equal incidence of breast and ovarian cancer.  
 CC A C to T substitution in exon 11 (position 4056 of the wild-type  
 CC BRCA1, see T18310) converted a Gln codon to a stop codon,  
 CC resulting in a BRCA1 polypeptide lacking 551 C-terminal residues.  
 CC cosegregation of the allele with disease and its absence in  
 CC controls were observed. Probes based on this and other  
 CC susceptibility alleles (see also T18312-14) can be used to  
 CC diagnose predisposition to cancer, partic. breast and ovarian  
 CC cancer.  
 SQ Sequence 5914 BP; 2006 A; 1155 C; 1316 G; 1437 T;

Query Match 99.9%; Score 5707.8; DB 1; Length 5914;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5709; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCTGGTGAAGCTCCGAGACCCCGACAGGCTGTGGGGTTCTCGATTAACCTGGCC 60  
DB 1 AGCTGGTGAAGCTCCGAGACCCCGACAGGCTGTGGGGTTCTCGATTAACCTGGCC 60

QY 61 CCGGCTGAGAGAGGCTTCAACCTCTGCTGTGGTAAAGTTTCATTTGAGAGAGAAA 120  
DB 61 CCGGCTGAGAGAGGCTTCAACCTCTGCTGTGGTAAAGTTTCATTTGAGAGAGAAA 120

QY 121 TGGATTTATCTGCTCTTCCGCTGGAAGAATGATTAATGCTATTAATGAGAAA 180  
DB 121 TGGATTTATCTGCTCTTCCGCTGGAAGAATGATTAATGCTATTAATGAGAAA 180

QY 181 TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGSACCTGTCCCAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGSACCTGTCCCAAGTGTGACC 240

QY 241 ACATATTTGCAAAATTTTGCATGCTGAACCTTCAACAGAGAGAGGCTTCAAGT 300  
DB 241 ACATATTTGCAAAATTTTGCATGCTGAACCTTCAACAGAGAGAGGCTTCAAGT 300

QY 301 GTCCCTTATGTAAGATGATATTAACCAAGAGGCTTCAAGAGAAATGAGATTAGTC 360  
DB 301 GTCCCTTATGTAAGATGATATTAACCAAGAGGCTTCAAGAGAAATGAGATTAGTC 360

QY 361 AACTGTGAGAGCTATGTAAGAAATGATTTGCTTTCACCTTGCACAGATTGGAGT 420  
DB 361 AACTGTGAGAGCTATGTAAGAAATGATTTGCTTTCACCTTGCACAGATTGGAGT 420

QY 421 ATGCAAAACAGCTATATTTTGCAAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
DB 421 ATGCAAAACAGCTATATTTTGCAAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480

QY 481 AAGTTTCTATCATCCAAAGATGAGGCTACAGAAACCGTCCAAAAGATCTTACAGAGTG 540  
DB 481 AAGTTTCTATCATCCAAAGATGAGGCTACAGAAACCGTCCAAAAGATCTTACAGAGTG 540

QY 541 AACCAGAAATCTCTCTTGGAGAAACGATGCTCAAGTCTCACTCTTAACCTTGGAA 600  
DB 541 AACCAGAAATCTCTCTTGGAGAAACGATGCTCAAGTCTCACTCTTAACCTTGGAA 600

QY 601 CTGTGAGAACTCTGAGGCAAGAGGCGGATACAACTCAAAAGAGCTGTCTACATGT 660  
DB 601 CTGTGAGAACTCTGAGGCAAGAGGCGGATACAACTCAAAAGAGCTGTCTACATGT 660

QY 661 AATTGGATCTGATTTCTTGAAGATACGTTAATAGGCAACTTATTTGAGTGGAG 720  
DB 661 AATTGGATCTGATTTCTTGAAGATACGTTAATAGGCAACTTATTTGAGTGGAG 720

QY 721 ATCAAGAAATTTTCAAAATCAACCCCTCAAGSACGAGGAGAAATCACTTGGATTCTG 780  
DB 721 ATCAAGAAATTTTCAAAATCAACCCCTCAAGSACGAGGAGAAATCACTTGGATTCTG 780

QY 781 CAAAAAGGCTGTGTAATTTTCTGAGAGGATGTAACAATTAATCTGAACATCAAC 840  
DB 781 CAAAAAGGCTGTGTAATTTTCTGAGAGGATGTAACAATTAATCTGAACATCAAC 840

QY 841 CCAGTAAATGATTTGAACACCACTGAGAGCGGTGAGAGGCGATCCAGAAAAGT 900  
DB 841 CCAGTAAATGATTTGAACACCACTGAGAGCGGTGAGAGGCGATCCAGAAAAGT 900

QY 901 ATCAGGAGTGTCTGTTCAAACTGATGAGGCACTGTGGCAAAATCTCATGTGCA 960  
DB 901 ATCAGGAGTGTCTGTTCAAACTGATGAGGCACTGTGGCAAAATCTCATGTGCA 960

QY 961 GCTCATTAACAGATGAGAGAGAGGATTTATTAATCACTAAAGAGAGATGATGAGAA 1020  
DB 961 GCTCATTAACAGATGAGAGAGAGGATTTATTAATCACTAAAGAGAGATGATGAGAA 1020

QY 1021 AGCTGAATTTCTGTAATTAAGCAAAAGAGGCTGGCTTACAGAGAGGCAACATTAACGAT 1080  
DB 1021 AGCTGAATTTCTGTAATTAAGCAAAAGAGGCTGGCTTACAGAGAGGCAACATTAACGAT 1080

QY 1081 GGGCTGGAATGAGGAAACATGTAATGATAGGCGGACTCCAGCAGAGAAAAAGGTAG 1140  
DB 1081 GGGCTGGAATGAGGAAACATGTAATGATAGGCGGACTCCAGCAGAGAAAAAGGTAG 1140

QY 1141 ATCTGAATGCTGATCCCGTGTGAGAGAAAAAGATGGAATTAACAGAAATGCTCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCGTGTGAGAGAAAAAGATGGAATTAACAGAAATGCTCATGCT 1200

QY 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATTAACCTTAATAGCAGATTGAGA 1260  
DB 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATTAACCTTAATAGCAGATTGAGA 1260

QY 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAACCTGTAAGTTCGATGACACATGATG 1320  
DB 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAACCTGTAAGTTCGATGACACATGATG 1320

QY 1321 GGGAGTCTGAATCAAAATGCAAAAGTACGTATGTTGAGAGTTCTAATGAGGTAGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCAAAAGTACGTATGTTGAGAGTTCTAATGAGGTAGATG 1380

QY 1381 AATATTCTGTTCTTCAAGAGAAATTAAGATTAAGCTTAAAGGCTTTAA 1440  
DB 1381 AATATTCTGTTCTTCAAGAGAAATTAAGATTAAGCTTAAAGGCTTTAA 1440

QY 1441 TATGTAAGAGGAAAGGTTTCACTCAAAATCAGTAGAGATTAATTAAGAGCAAAATAT 1500  
DB 1441 TATGTAAGAGGAAAGGTTTCACTCAAAATCAGTAGAGATTAATTAAGAGCAAAATAT 1500

QY 1501 TTGGGAAACCTATCGAGAGAGGCAAGCCCTCCCAACTTAAGCCATTAAGTAAATC 1560  
DB 1501 TTGGGAAACCTATCGAGAGAGGCAAGCCCTCCCAACTTAAGCCATTAAGTAAATC 1560

QY 1561 TAATTATGAGAGCTTTGTTACTGAGCCACAGATTAATTAAGAGGCTCCCTCAAAATA 1620  
DB 1561 TAATTATGAGAGCTTTGTTACTGAGCCACAGATTAATTAAGAGGCTCCCTCAAAATA 1620

QY 1621 AATTAAAGCGTAAAGAGAGGCTCACTCAGGCTTCAACCGTAGAGATTTATCAAGAAAG 1680  
DB 1621 AATTAAAGCGTAAAGAGAGGCTCACTCAGGCTTCAACCGTAGAGATTTATCAAGAAAG 1680

QY 1681 CAGATTTGGCAGTTCAAAAGAGCTCTGAAATGATTAATCAAGGAACTTAACCAAGGAGC 1740  
DB 1681 CAGATTTGGCAGTTCAAAAGAGCTCTGAAATGATTAATCAAGGAACTTAACCAAGGAGC 1740

QY 1741 AGAATGCTCAAGTGAATTTTCTAATAGTGTCTATGAGATTAACCAAGAGGATTT 1800  
DB 1741 AGAATGCTCAAGTGAATTTTCTAATAGTGTCTATGAGATTAACCAAGAGGATTT 1800

QY 1801 CTATTGGAATGAGAAAAATCTTAACCAATAGAAATACGAGAAAAAGATCTGTTCA 1860  
DB 1801 CTATTGGAATGAGAAAAATCTTAACCAATAGAAATACGAGAAAAAGATCTGTTCA 1860

QY 1861 AAAGGAAAGCTGAACCTTAAGAGAGGAGTATTAAGCAATATGAGAACTGAAATTAATATCC 1920  
DB 1861 AAAGGAAAGCTGAACCTTAAGAGAGGAGTATTAAGCAATATGAGAACTGAAATTAATATCC 1920

QY 1921 ACAATTAAGAGCACTTAAGAAAGATAGGCTGAGAGAGAGTCTTCAACAGGATATTC 1980  
DB 1921 ACAATTAAGAGCACTTAAGAAAGATAGGCTGAGAGAGAGTCTTCAACAGGATATTC 1980

QY 1981 ATGGGCTTGAACCTGATGATGAGAAATCTAAGCCACGCTAATTTGATGAAATGAGAA 2040  
DB 1981 ATGGGCTTGAACCTGATGATGAGAAATCTAAGCCACGCTAATTTGATGAAATGAGAA 2040

QY 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAGTAAACCAATATGCACTCA 2100  
DB 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAGTAAACCAATATGCACTCA 2100

QY 2101 GGCACAGCAGAAACCTTAACACTATGGAAGTAAAGAACTGCAACTGGAGCCAGAGAA 2160

```

|||||
Db 2101 GGGACGACAAAACCTACCACTCATGAGGTAAGAACTGCACTGAGACCGCAAGAA 2160
QY 2161 GTACACAGCCAAATGACAGACAACTAAAAGACATGACAGGACTACTTCCAGAGCTGA 2220
Db 2161 GTACACAGCCAAATGACAGACAACTAAAAGACATGACAGGACTACTTCCAGAGCTGA 2220
QY 2221 AGTTAACAAATGCACTGCTGTTCTTTACTAAGTGTCAAAATACCACTGAACCTTAAAGAT 2280
Db 2221 AGTTAACAAATGCACTGCTGTTCTTTACTAAGTGTCAAAATACCACTGAACCTTAAAGAT 2280
QY 2281 TTGTCAATCCTAGCCTTCCAGAGAAAAGAAAAGAACTGAACATTAAGT 2340
Db 2281 TTGTCAATCCTAGCCTTCCAGAGAAAAGAAAAGAACTGAACATTAAGT 2340
QY 2341 CTATATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAACTG 2400
Db 2341 CTATATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAACTG 2400
QY 2401 AAGATCTGTAGAGAGTAGAGATTTTCATTGGTACCTGGTACTGATTATGCGACTCAGG 2460
Db 2401 AAGATCTGTAGAGAGTAGAGATTTTCATTGGTACCTGGTACTGATTATGCGACTCAGG 2460
QY 2461 AAGATCTGTAGAGAGTAGAGATTTTCATTGGTACCTGGTACTGATTATGCGACTCAGG 2520
Db 2461 AAGATCTGTAGAGAGTAGAGATTTTCATTGGTACCTGGTACTGATTATGCGACTCAGG 2520
QY 2521 GTGTGAGTCAGTGTGCGACATTTGAAAACCCCAAGGACTAATTCATGTTGTTCCAAAG 2580
Db 2521 GTGTGAGTCAGTGTGCGACATTTGAAAACCCCAAGGACTAATTCATGTTGTTCCAAAG 2580
QY 2581 ATATATGAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAACACAGTC 2640
Db 2581 ATATATGAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAACACAGTC 2640
QY 2641 GGGAAAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCACTATTTGCGAATACAT 2700
Db 2641 GGGAAAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCACTATTTGCGAATACAT 2700
QY 2701 TCAGAGTTTCAAAAGCCGCACTATTTGCTGTGTTTCAAAATCCAGAAATGCGAAGAGG 2760
Db 2701 TCAGAGTTTCAAAAGCCGCACTATTTGCTGTGTTTCAAAATCCAGAAATGCGAAGAGG 2760
QY 2761 AATGTGCAACATTTCTGTGCCCACTCTGGGTCCTTAAGAAACAAGTCCAAAGTCACTT 2820
Db 2761 AATGTGCAACATTTCTGTGCCCACTCTGGGTCCTTAAGAAACAAGTCCAAAGTCACTT 2820
QY 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGATGAGTCTAATATATCAAGCTGTAC 2880
Db 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGATGAGTCTAATATATCAAGCTGTAC 2880
QY 2881 ACACAGTTAATATCACTGCGAGGCTTTCCTGTGTGTTGTCAGAAAATATACCCAGTTGATA 2940
Db 2881 ACACAGTTAATATCACTGCGAGGCTTTCCTGTGTGTTGTCAGAAAATATACCCAGTTGATA 2940
QY 2941 ATGCCAAATGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCACTTCAGAGCA 3000
Db 2941 ATGCCAAATGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCACTTCAGAGCA 3000
QY 3001 ACGAAACTGAGACTATTAATTAACATGAGCTTTTACAAAACCCATATCGTATAC 3060
Db 3001 ACGAAACTGAGACTATTAATTAACATGAGCTTTTACAAAACCCATATCGTATAC 3060
QY 3061 CACCACTTTTCCCACTCAAGTCAATTTGTTAAACTTAATGTAGAAAAAATCTGTAGAGG 3120
Db 3061 CACCACTTTTCCCACTCAAGTCAATTTGTTAAACTTAATGTAGAAAAAATCTGTAGAGG 3120
QY 3121 AAAACTTTGAGGAACCTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAATTCGAA 3180
Db 3121 AAAACTTTGAGGAACCTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAATTCGAA 3180
QY 3181 GTACAGTGAACAATTAACCGTAAATACATTAAGAAAATGTTTTTAAGAGCGACGT 3240
Db 3181 GTACAGTGAACAATTAACCGTAAATACATTAAGAAAATGTTTTTAAGAGCGACGT 3240

|||||
Db 3181 GTACAGTGAACAATTAACCGTAAATACATTAAGAAAATGTTTTTAAGAGCGACGT 3240
QY 3241 CAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGTGGGCTCCAGATTAATGAAG 3300
Db 3241 CAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGTGGGCTCCAGATTAATGAAG 3300
QY 3301 TAGGTTCACTGATGAAGAACTTCAAGCAGACTAGCTAGTGAAGAGAGGCCAAATTTGA 3360
Db 3301 TAGGTTCACTGATGAAGAACTTCAAGCAGACTAGCTAGTGAAGAGAGGCCAAATTTGA 3360
QY 3361 ATGCTATGCTTAGATTAAGGGGTTTGGAACTAGGCTATATAACAAAGTCTCCGGA 3420
Db 3361 ATGCTATGCTTAGATTAAGGGGTTTGGAACTAGGCTATATAACAAAGTCTCCGGA 3420
QY 3421 GTAAATGTGAACATCTGAAATAAAAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTTA 3480
Db 3421 GTAAATGTGAACATCTGAAATAAAAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTTA 3480
QY 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATTAATTAACAGCTATGGAAGTAGTC 3540
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATTAATTAACAGCTATGGAAGTAGTC 3540
QY 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGAATTAAG 3600
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGAATTAAG 3600
QY 3601 AAGATACTAGTTTGTCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTCGAAAAGCG 3660
Db 3601 AAGATACTAGTTTGTCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTCGAAAAGCG 3660
QY 3661 TCCAGAAAGAGAGCTTAGCAGAGTCCTAGGCCCTTTCACCCATACACTTGGCTCAGG 3720
Db 3661 TCCAGAAAGAGAGCTTAGCAGAGTCCTAGGCCCTTTCACCCATACACTTGGCTCAGG 3720
QY 3721 GTTACCGAAGAGGAGGCGCAAGAAATTAAGTCTCAGAGAAAGAACTAATTAAGTAGAGATG 3780
Db 3721 GTTACCGAAGAGGAGGCGCAAGAAATTAAGTCTCAGAGAAAGAACTAATTAAGTAGAGATG 3780
QY 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTTAAAGTAAACAATATACCTTCACT 3840
Db 3781 AAGAGCTTCCCTGCTTCCAAACACTTGTATTTGTTAAAGTAAACAATATACCTTCACT 3840
QY 3841 CTACTAGGCAATACACCGTGTGCTACCGAGTGTCTGTCTAAGAACACAGAGGAATTAAT 3900
Db 3841 CTACTAGGCAATACACCGTGTGCTACCGAGTGTCTGTCTAAGAACACAGAGGAATTAAT 3900
QY 3901 TATCATTGAAGAAATAGCTTAATTAATGACTGAGTACAGAGTAATATTTGGCAAAAGCATCTC 3960
Db 3901 TATCATTGAAGAAATAGCTTAATTAATGACTGAGTACAGAGTAATATTTGGCAAAAGCATCTC 3960
QY 3961 AGGACATCACTTAAGTAGAGAAACAAAATGTTGCTAGCTTGTCTTCCACAGTGA 4020
Db 3961 AGGACATCACTTAAGTAGAGAAACAAAATGTTGCTAGCTTGTCTTCCACAGTGA 4020
QY 4021 GTGAATTTGAAGACTGACTGCAAAATACAAACACCAGAGATCTTCTGTGATGTTTCTT 4080
Db 4021 GTGAATTTGAAGACTGACTGCAAAATACAAACACCAGAGATCTTCTGTGATGTTTCTT 4080
QY 4081 CCAAAACAATGAGGCACTGACTGAAAGCCAGGAGTTGTTCTGATGATACAGAAATGG 4140
Db 4081 CCAAAACAATGAGGCACTGACTGAAAGCCAGGAGTTGTTCTGATGATACAGAAATGG 4140
QY 4141 TTTCAATGATGAAGAAAGAGAGAGGAGGCTTGAAGAAAATATATCAAGAGCAAAAGCA 4200
Db 4141 TTTCAATGATGAAGAAAGAGAGAGGAGGCTTGAAGAAAATATATCAAGAGCAAAAGCA 4200
QY 4201 TGGATTCAAACTTAGTGAAGCAGATCTGGGTGGAAGAGTGAAGCAAGCCTCTCTGAAG 4260
Db 4201 TGGATTCAAACTTAGTGAAGCAGATCTGGGTGGAAGAGTGAAGCAAGCCTCTCTGAAG 4260
QY 4261 ACTGCTCAGGAGTATCCTCTGAGAGTGAATTAACCACTCAGCAGAGGATACCATGC 4320
Db 4261 ACTGCTCAGGAGTATCCTCTCAGAGTGAATTAACCACTCAGCAGAGGATACCATGC 4320
```



QY 4321 AACATACCTGATTAAGCTCCAGCAGAAATGGCTGACTAGATGAGTGTGTAGAACACG 4380  
 DB 4321 AACATACCTGATTAAGCTCCAGCAGAAATGGCTGACTAGATGAGTGTGTAGAACACG 4380  
 QY 4381 ATGGAGCCGACCTTCTTAACAGCTACCTTCCATCAATAGTACTCTTGCCCTTGAGG 4440  
 DB 4381 ATGGAGCCGACCTTCTTAACAGCTACCTTCCATCAATAGTACTCTTGCCCTTGAGG 4440  
 QY 4441 ACCTGGGAAATCCAGAACAGACATCAGAAAAAGCAGTATTAACTTCACAGAAAAATGA 4500  
 DB 4441 ACCTGGGAAATCCAGAACAGACATCAGAAAAAGCAGTATTAACTTCACAGAAAAATGA 4500  
 QY 4501 GTGAATACCTTAATAGCAGAAATCCAGAGCCCTTCTGCTGACAGTGTAGTGTCTG 4560  
 DB 4501 GTGAATACCTTAATAGCAGAAATCCAGAGCCCTTCTGCTGACAGTGTAGTGTCTG 4560  
 QY 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620  
 DB 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620  
 QY 4621 GCCCATCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
 DB 4621 GCCCATCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
 QY 4681 ACTACCATCATTAAGAGAGAGTCTTAATAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4740  
 DB 4681 ACTACCATCATTAAGAGAGAGTCTTAATAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4740  
 QY 4741 AGTCTGGGACACAGATTTAGCGAAACATCTTACTGCCAAGCAGATCTAGAGGAA 4800  
 DB 4741 AGTCTGGGACACAGATTTAGCGAAACATCTTACTGCCAAGCAGATCTAGAGGAA 4800  
 QY 4801 CCCCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4860  
 DB 4801 CCCCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4860  
 QY 4861 AAGACAGAGCCCGACAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4920  
 DB 4861 AAGACAGAGCCCGACAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4920  
 QY 4921 AAGTCCCAATTAAGAGTGAAGTGTGCGAAGTCCAGTGGCTGCTCATTAATCTG 4980  
 DB 4921 AAGTCCCAATTAAGAGTGAAGTGTGCGAAGTCCAGTGGCTGCTCATTAATCTG 4980  
 QY 4981 ATACTGCTGGTATTAATGCAATGGAAGAGTGTGAGCAGAGAGAACCCAGAAATGACAG 5040  
 DB 4981 ATACTGCTGGTATTAATGCAATGGAAGAGTGTGAGCAGAGAGAACCCAGAAATGACAG 5040  
 QY 5041 CTTCACACAGAGGGTCAACAAAAGAAATGTCATGTGTGTGTGTGTGTGTGTGTGTGTGT 5100  
 DB 5041 CTTCACACAGAGGGTCAACAAAAGAAATGTCATGTGTGTGTGTGTGTGTGTGTGTGTGT 5100  
 QY 5101 AATTATGCTGCTGATCAATTTGCGAAGAACCAACATCACTTAATTAATTAATTAATTA 5160  
 DB 5101 AATTATGCTGCTGATCAATTTGCGAAGAACCAACATCACTTAATTAATTAATTAATTA 5160  
 QY 5161 CTGAAGAGACTACTCATGTTGTATGAAAAAGATGCTGAGTTGTGTGTGTGTGTGTGTGTGT 5220  
 DB 5161 CTGAAGAGACTACTCATGTTGTATGAAAAAGATGCTGAGTTGTGTGTGTGTGTGTGTGTGT 5220  
 QY 5221 TGAATATTTTCTAGAGAAATGCGGAGAGAAATGAGTGTGTGTGTGTGTGTGTGTGTGTGT 5280  
 DB 5221 TGAATATTTTCTAGAGAAATGCGGAGAGAAATGAGTGTGTGTGTGTGTGTGTGTGTGTGT 5280  
 QY 5281 AGCTATTTAAGAAAGAAATGCTGAAATGAGATGATTTGAAAGTCAAGAGAGAGTGTGTGTGTGT 5340  
 DB 5281 AGCTATTTAAGAAAGAAATGCTGAAATGAGATGATTTGAAAGTCAAGAGAGAGTGTGTGTGTGT 5340  
 QY 5341 TCATGGAAGAAACCAAGAGTCCAAAGCAGAGAGAGAGATCCAGAGAGAGAGATCT 5400  
 DB 5341 TCATGGAAGAAACCAAGAGTCCAAAGCAGAGAGAGAGATCCAGAGAGAGAGATCT 5400

QY 5401 TCAGGGGGCTAGAAATCTGTGCTATGGGCTTCACCAACATGCCACAGATCAACTGG 5460  
 DB 5401 TCAGGGGGCTAGAAATCTGTGCTATGGGCTTCACCAACATGCCACAGATCAACTGG 5460  
 QY 5461 AATGATGTGACAGCTGT 5520  
 DB 5461 AATGATGTGACAGCTGT 5520  
 QY 5521 GCACAGGTGTCCACCAATTTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5580  
 DB 5521 GCACAGGTGTCCACCAATTTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5580  
 QY 5581 TCCATGCAATTTGGGAGATGT 5640  
 DB 5581 TCCATGCAATTTGGGAGATGT 5640  
 QY 5641 GTGTAGCAGCTCTACAGAGTCCAGAGAGTGGACCTGATGATGATGATGATGATGATGATG 5700  
 DB 5641 GTGTAGCAGCTCTACAGAGTCCAGAGAGTGGACCTGATGATGATGATGATGATGATGATG 5700  
 QY 5701 GCCACTACTGA 5711  
 DB 5701 GCCACTACTGA 5711  
 RESULT 15  
 ID T18313 standard; cDNA; 5914 BP.  
 AC T18313;  
 DT 05-JUN-1996 (first entry)  
 DE BRCA1 gene missense allele.  
 KW BRCA1; breast cancer; ovary cancer; predisposing gene;  
 KM susceptibility gene; diagnosis; prognosis; allele; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT cds 120..5711  
 FT /\*tag- a  
 FT allele 5443  
 FT /\*tag- b  
 FT /\*note- "t at position 5443 of wild-type  
 FT BRCA1 is substituted by g"  
 PN MO9605307-A2.  
 PD 22-FEB-1996.  
 PE 11-AUG-1995; 010203.  
 PR 12-AUG-1994; US-289221.  
 PR 02-SEP-1994; US-300266.  
 PR 16-SEP-1994; US-308104.  
 PR 29-NOV-1994; US-348824.  
 PR 24-MAR-1995; US-409305.  
 PR 07-JUN-1995; US-488011.  
 PR 07-JUN-1995; US-483554.  
 PR 07-JUN-1995; US-487002.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PA (UTAH-) UNIV UTAH RES FOUND.  
 PA (USSR-) US DEPT HEALTH & HUMAN SERVICES.  
 PA Futrelle AP, Goldgar DE, Hartsman KD, Kamb A, Miki Y;  
 PI Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV;  
 PI Wiseman RW;  
 DR MPI: 96-139703/14.  
 PT New isolated human cancer predisposing gene, BRCA1 - used to develop  
 PT prods. for diagnosis, prognosis and therapy of cancers, partic.  
 PT breast and ovarian cancers  
 PS Claim 9; Page 108-117; 190pp; English.  
 CC A BRCA1 susceptibility allele (T18313) was detected in a kindred  
 CC that displayed early age of breast cancer onset. A T to G  
 CC mutation in exon 21 (position 5443 in the wild-type BRCA1  
 CC gene, see T18310) is potentially disruptive as it causes the  
 CC replacement of small, hydrophobic Met by large, charged Arg.  
 CC cosegregation of the allele with disease and its absence in  
 CC controls were observed. Probes based on this and other  
 CC susceptibility alleles (see also T18311-12 and T18314) can be  
 CC used to diagnose predisposition to cancer, partic. breast and  
 CC ovarian cancer.

Seq	Sequence	5914 BP;	2006 A;	1156 C;	1317 G;	1435 T;
Query Match 99.9%; Score 5707.8; DB 1; Length 5914;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 5709; Conservative 0; Mismatches 2; Indels 0; Gaps 0;						
OY	1	ACGTGCTGAGACTTCTCTGGAGCCCGCACCAGGCTGTGGGGTTTCTAGATTAACGTGGGCC	60			
Db	1	ACGTGCTGAGACTTCTCTGGAGCCCGCACCAGGCTGTGGGGTTTCTAGATTAACGTGGGCC	60			
OY	61	CTGCGCTCAGAGAGCCCTTACCCCTGCTCTGGGTAAATTCATTGGAACAGAAAAAA	120			
Db	61	CTGCGCTCAGAGAGCCCTTACCCCTGCTCTGGGTAAATTCATTGGAACAGAAAAAA	120			
OY	121	TGAGTTATCTGCTCTTCCGCTTGAAGAAAGTACAAAATGCTATTAATGCTATGCAGAAAA	180			
Db	121	TGAGTTATCTGCTCTTCCGCTTGAAGAAAGTACAAAATGCTATTAATGCTATGCAGAAAA	180			
OY	181	TCTTAGAGTGTCCCATCTGCTCTGGAGTTGATCAAGAACTGTCTCCAAAGTGTGACC	240			
Db	181	TCTTAGAGTGTCCCATCTGCTCTGGAGTTGATCAAGAACTGTCTCCAAAGTGTGACC	240			
OY	241	ACATATTTTGAACAATTTTGGATGCTGAAGTCTCAACGAGAAAGAGGCGCTTACAGT	300			
Db	241	ACATATTTTGAACAATTTTGGATGCTCAAACTTCTCAACGAGAAAGAGGCGCTTACAGT	300			
OY	301	GTCCTTATGTAAGATGATATACCAAAAGAGCCTACAAAGAAAGTACAGATTTTATGTC	360			
Db	301	GTCCTTATGTAAGATGATATACCAAAAGAGCCTACAAAGAAAGTACAGATTTTATGTC	360			
OY	361	AACTTGTGAAGAGCTATGAAAAATCATTTGTCTTTTCAAGCTTGACACAGGTTGGAGT	420			
Db	361	AACTTGTGAAGAGCTATGAAAAATCATTTGTCTTTTCAAGCTTGACACAGGTTGGAGT	420			
OY	421	ATGCAACAGCTATATATTTTGCAAAAAGAAATATACCTCTCTGAACATCTAAAAAGATG	480			
Db	421	ATGCAACAGCTATATATTTTGCAAAAAGAAATATACCTCTCTGAACATCTAAAAAGATG	480			
OY	481	AACTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540			
Db	481	AACTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540			
OY	541	AACCGGAAATCTCTCCGCAAGGAACCAAGTCTCACTGCTCAACCTTCTGAACTTGGAA	600			
Db	541	AACCGGAAATCTCTCTCCGCAAGGAACCAAGTCTCACTGCTCAACCTTCTGAACTTGGAA	600			
OY	601	CTGTGAGAACTCTGAGGACAAAGCAGCGATACAACTCTCAAAAGAGCTGTCTACATTG	660			
Db	601	CTGTGAGAACTCTGAGGACAAAGCAGCGATACAACTCTCAAAAGAGCTGTCTACATTG	660			
OY	661	AATGGGATCTGATCTTCTGAAGATACCGTTAATAAGCAACTTATGCAAGTGGGAG	720			
Db	661	AATGGGATCTGATCTTCTGAAGATACCGTTAATAAGCAACTTATGCAAGTGGGAG	720			
OY	721	ATCAGAAATTTTAAACCAACCCCTCAAGGAACCAAGGATGAATTAACAGTTTGGATCTG	780			
Db	721	ATCAGAAATTTTAAACCAACCCCTCAAGGAACCAAGGATGAATTAACAGTTTGGATCTG	780			
OY	781	CAAAAAGGCTCTGTGAAATTTTCTGAGACGGATTAACAATTAATCTGAACATCATCAAC	840			
Db	781	CAAAAAGGCTCTGTGAAATTTTCTGAGACGGATTAACAATTAATCTGAACATCATCAAC	840			
OY	841	CCAGTAATTAATGATTTGAACACCACTGAGAGCGTGACGTGAGAGCATCCAGAAAAGT	900			
Db	841	CCAGTAATTAATGATTTGAACACCACTGAGAGCGTGACGTGAGAGCATCCAGAAAAGT	900			
OY	901	ATCAGGATGTTCTGTTCAAACTTGCATGTGAGCCATGTGGCAAAAATACCATGCA	960			
Db	901	ATCAGGATGTTCTGTTCAAACTTGCATGTGAGCCATGTGGCAAAAATACCATGCA	960			
OY	961	GCTCATTCAGCATGAGAAACAGAGTTTATTACTCACTAAAGCAGAAATGAATGTAGAAA	1020			
Db	961	GCTCATTCAGCATGAGAAACAGAGTTTATTACTCACTAAAGCAGAAATGAATGTAGAAA	1020			
OY	1021	AGGCTGAATTTCTGTAATTAAGCAACAGCCCTGGCTTAGCAAGGAGCCAACTAACAGAT	1080			
Db	1021	AGGCTGAATTTCTGTAATTAAGCAACAGCCCTGGCTTAGCAAGGAGCCAACTAACAGAT	1080			
OY	1081	GGGCTGGAAGTAAAGAAACATGATGATAGGCGACCTCCCGACACAGAAAAAGGTAG	1140			
Db	1081	GGGCTGGAAGTAAAGAAACATGATGATAGGCGACCTCCCGACACAGAAAAAGGTAG	1140			
OY	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATAGCAAGAACTGCCATGCT	1200			
Db	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATAGCAAGAACTGCCATGCT	1200			
OY	1201	CAGAGAACTCTAGAGATGATGAGATGTTCTTGGATTAACACTAAATAGCAGCATTCAGA	1260			
Db	1201	CAGAGAACTCTAGAGATGATGAGATGTTCTTGGATTAACACTAAATAGCAGCATTCAGA	1260			
OY	1261	AACTTAATGAGTGTGTTTCCAGAAAGTGAACCTGTAGGTTCTGATGACTACATGATG	1320			
Db	1261	AACTTAATGAGTGTGTTTCCAGAAAGTGAACCTGTAGGTTCTGATGACTACATGATG	1320			
OY	1321	GGGAGCTGAATCAAAATGCCAAAGTAGCTGATGATTTGAGAGTTCTTAATAGGTAGATG	1380			
Db	1321	GGGAGCTGAATCAAAATGCCAAAGTAGCTGATGATTTGAGAGTTCTTAATAGGTAGATG	1380			
OY	1381	AAATTTCTGTTCTTCCAGAAAAATAGACTTACTGGCCAGTATCTCATGAGGCTTTAA	1440			
Db	1381	AAATTTCTGTTCTTCCAGAAAAATAGACTTACTGGCCAGTATCTCATGAGGCTTTAA	1440			
OY	1441	TATGTAAAGTGAAGAGTCTCCCAATCAGTGAAGATATTTGAAGCAAAATAT	1500			
Db	1441	TATGTAAAGTGAAGAGTCTCCCAATCAGTGAAGATATTTGAAGCAAAATAT	1500			
OY	1501	TTGGGAAACCTATCGGAAGAGGAGGAGGCTCCCACTTAAGCCATGTAACGAAAAATC	1560			
Db	1501	TTGGGAAACCTATCGGAAGAGGAGGAGGCTCCCACTTAAGCCATGTAACGAAAAATC	1560			
OY	1561	TAAATTAAGGACATTTGTTACTGAGCCACAGATATATCAAGAGGCTCCCTCAAAATA	1620			
Db	1561	TAAATTAAGGACATTTGTTACTGAGCCACAGATATATCAAGAGGCTCCCTCAAAATA	1620			
OY	1621	AAATTAAGGCTAAAGAGAACTACATAGGCTTCATCCGAGATTTTATCAAGAAAG	1680			
Db	1621	AAATTAAGGCTAAAGAGAACTACATAGGCTTCATCCGAGATTTTATCAAGAAAG	1680			
OY	1681	CAGATTTGCGACTTCAAAAAGACTCCTGAATGATTAATCAGGAACTAACCAAAACGAGC	1740			
Db	1681	CAGATTTGCGACTTCAAAAAGACTCCTGAATGATTAATCAGGAACTAACCAAAACGAGC	1740			
OY	1741	AGAATGCTCAAGTGAATTAATTAATAGTGTATGAGATTAATAACAAAGGTGATT	1800			
Db	1741	AGAATGCTCAAGTGAATTAATTAATAGTGTATGAGATTAATAACAAAGGTGATT	1800			
OY	1801	CTATTCAAGATGAGAAAAATCTTAACCAATAGAACTCTGAAAAAATAATCTGTTTCA	1860			
Db	1801	CTATTCAAGATGAGAAAAATCTTAACCAATAGAACTCTGAAAAAATAATCTGTTTCA	1860			
OY	1861	AAACGAAAGCTGAACCTATTAAGCAGCAGTATTAAGCAATATGGAATTCGAATATATCC	1920			
Db	1861	AAACGAAAGCTGAACCTATTAAGCAGCAGTATTAAGCAATATGGAATTCGAATATATCC	1920			
OY	1921	ACAATTCAAAACACCTTAATAAGGCTGAGAGGAAGTCTTCTACAGGATATTC	1980			
Db	1921	ACAATTCAAAACACCTTAATAAGGCTGAGAGGAAGTCTTCTACAGGATATTC	1980			
OY	1981	ATGCGCTTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2040			
Db	1981	ATGCGCTTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2040			
OY	2041	TTGATAGTGTCTAGCAGTGAAGATTAAGAAAAAATTAACCAAAATGCGCAGTCA	2100			
Db	2041	TTGATAGTGTCTAGCAGTGAAGATTAAGAAAAAATTAACCAAAATGCGCAGTCA	2100			

QY	2101	GGGACACAGAAACCTCAGCAACCTCATGGAAGGTAAAGAAACCTCCAACTGAGCAAGAAAGA	2160
Db	2101	GGCACACAGAAACCTCAGCAACCTCATGGAAGGTAAAGAAACCTCCAACTGAGCAAGAAAGA	2160
QY	2161	GTAAACAAGCCAAATGAAACAGACAAAGTAAAGACATGACAGCATCTACTTCCAGAGCTGA	2230
Db	2161	GTAAACAAGCCAAATGAAACAGACAAAGTAAAGACATGACAGCATCTACTTCCAGAGCTGA	2230
QY	2281	TTTGCAATCCTTACCTTCCAGAGGAAGAAAAGAGAGAAATACAAAACGTAAAGAGT	2340
Db	2281	TTTGCAATCCTTACCTTCCAGAGGAAGAAAAGAGAGAAATACAAAACGTAAAGAGT	2340
QY	2341	CTATAATGCTGAGAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTGGCAACTG	2400
Db	2341	CTATAATGCTGAGAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTGGCAACTG	2400
QY	2401	AAGATCTGCTGCTACTGAGAACTGACACCTCTAGAGGAGCAGAAAACAGAACCAATTAAT	2460
Db	2401	AAGATCTGCTGCTACTGAGAACTGACACCTCTAGAGGAGCAGAAAACAGAACCAATTAAT	2460
QY	2461	AAAGTATCTGCTGCTACTGAGAACTGACACCTCTAGAGGAGCAGAAAACAGAACCAATTAAT	2520
Db	2461	AAAGTATCTGCTGCTACTGAGAACTGACACCTCTAGAGGAGCAGAAAACAGAACCAATTAAT	2520
QY	2521	GTTGTAGTCACTGTGTGACGACATTTGAAAACCCCAAGGAGCAATTCATGTTGCCAAG	2580
Db	2521	GTTGTAGTCACTGTGTGACGACATTTGAAAACCCCAAGGAGCAATTCATGTTGCCAAG	2580
QY	2581	ATATAATGAATGACACAGAGAGGCTTTAATATTCATCTGAGGACATGAATTAACACAGCTC	2640
Db	2581	ATATAATGAATGACACAGAGAGGCTTTAATATTCATCTGAGGACATGAATTAACACAGCTC	2640
QY	2641	GGGAAACAAACATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGGCAGATACAT	2700
Db	2641	GGGAAACAAACATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGGCAGATACAT	2700
QY	2701	TCAAGGTTTCAAGCCCGCCAGCTATTGGTCTCTGTTTTCAAAATCCAGAGAAATGCAGAAAGG	2760
Db	2701	TCAAGGTTTCAAGCCCGCCAGCTATTGGTCTCTGTTTTCAAAATCCAGAGAAATGCAGAAAGG	2760
QY	2761	AATGTGCACATCTCTGTGCCACTCTGSGTCCCTTAAGAAACAAAGTCCCAAAAGTCACTT	2820
Db	2761	AATGTGCACATCTCTGTGCCACTCTGSGTCCCTTAAGAAACAAAGTCCCAAAAGTCACTT	2820
QY	2821	TTGAAATGTGAACAAAAGGAAGAAATCAGAGAAAGATGAGTCTAATATCAAGCTGTAC	2880
Db	2821	TTGAAATGTGAACAAAAGGAAGAAATCAGAGAAAGATGAGTCTAATATCAAGCTGTAC	2880
QY	2881	AGACAGTAAATATCAGTCGAGGCTTCCGTGSGTGGTCAGAGAAATATAGCCAGTGTATA	2940
Db	2881	AGACAGTAAATATCAGTCGAGGCTTCCGTGSGTGGTCAGAGAAATATAGCCAGTGTATA	2940
QY	2941	ATGCCAATGTAGTATCAAGAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCCAGAGCA	3000
Db	2941	ATGCCAATGTAGTATCAAGAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCCAGAGCA	3000
QY	3001	ACGAAATCGACATCTTACCTCCAAATTAACATGAGCACTTTTCCAAAACCCCAATGCTATAC	3060
Db	3001	ACGAAATCGACATCTTACCTCCAAATTAACATGAGCACTTTTCCAAAACCCCAATGCTATAC	3060
QY	3061	CACACATTTTCCCATCAAGTACTTTGTTAAACATTAATGTAAAGAAATGTGCTAGAGG	3120
Db	3121	AAAACCTTTGAGGAACATTCATATGTCACTCAGTAAAGAGAAATGGAAATGAGAACATTCGAA	3180
QY	3121	AAAACCTTTGAGGAACATTCATATGTCACTCAGTAAAGAGAAATGGAAATGAGAACATTCGAA	3180

QY	3181	GTACAGGACACAATAGCCGCTAATACATTAGAGAAAGTTTAAAGACGACGT	3240
Db	3181	GTACAGGACACAATTAGGCCCTAATACATTAGAGAAAGTTTAAAGACGACGT	3240
QY	3241	CAACCAATATTAATGAAGTAGTTCACAGTAAATGAAGTGGGCTCCAGTATTAATGA	3300
Db	3241	CAACCAATATTAATGAAGTAGTTCACAGTAAATGAAGTGGGCTCCAGTATTAATGA	3300
QY	3301	TAGGTTCCAGTAGTAAGAAACATTCAAGACAGAACTAGTAGAAACAGAGGCCAAATTTGA	3360
Db	3301	TAGGTTCCAGTAGTAAGAAACATTCAAGACAGAACTAGTAGAAACAGAGGCCAAATTTGA	3360
QY	3361	ATGCTATGCTTAGATTAGGGGTTTTGCCAACCTGAGGTCTATAACAAAGTCTTCTGGAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCCAACCTGAGGTCTATAACAAAGTCTTCTGGAA	3420
QY	3421	GTAATTTGTAAGCACTCCGAATTAATAAACAGAAATATTAACAGTACTGACACTGTA	3480
Db	3421	GTAATTTGTAAGCACTCCGAATTAATAAACAGAAATATTAACAGTACTGACACTGTA	3480
QY	3481	ATACAGATTTCTCCTCATATCTGATTTACAGATTAACCTAGAACAGCCTATGGAAAGTAC	3540
Db	3481	ATACAGATTTCTCCTCATATCTGATTTACAGATTAACCTAGAACAGCCTATGGAAAGTAC	3540
QY	3541	ATGCATCTCAGGTTTGTCTCGACACCTGATGACCTGTTAGATATGCTGAATAAAG	3600
Db	3541	ATGCATCTCAGGTTTGTCTCGACACCTGATGACCTGTTAGATATGCTGAATAAAG	3600
QY	3601	AAAGATCTAGTTTGGCGAAATGACATTAAGAAAGTCTGCTGTTTTAGCAAAACG	3660
Db	3601	AAAGATCTAGTTTGGCGAAATGACATTAAGAAAGTCTGCTGTTTTAGCAAAACG	3660
QY	3661	TCCAGAAAGGAGAGCTTAGCAGAGAGTCTTAGCCCTTTCACCCATACATTTGGCTCAG	3720
Db	3661	TCCAGAAAGGAGAGCTTAGCAGAGAGTCTTAGCCCTTTCACCCATACATTTGGCTCAG	3720
QY	3721	GTTACCCGAAGGGGCCAAGAAATTAGAGTCTCAGAGAGACTTATCTAGTGAATG	3780
Db	3721	GTTACCCGAAGGGGCCAAGAAATTAGAGTCTCAGAGAGACTTATCTAGTGAATG	3780
QY	3781	AAGAGCTCCCTGCTTCCAACTGTTTATTTGGTAAGTAACAATATACCTCTCAGT	3840
Db	3781	AAGAGCTCCCTGCTTCCAACTGTTTATTTGGTAAGTAACAATATACCTCTCAGT	3840
QY	3841	CTATAGGACATAGCACCGTGTCTACGAGTGTCTGTCTAAGAACACAGAGAGATTTAT	3900
Db	3841	CTATAGGACATAGCACCGTGTCTACGAGTGTCTGTCTAAGAACACAGAGAGATTTAT	3900
QY	3901	TATCATTTGAAGAAATAGCTTAATAGACTGCACTAGACAGTAAATATGGCAAAAGCATCTC	3960
Db	3901	TATCATTTGAAGAAATAGCTTAATAGACTGCACTAGACAGTAAATATGGCAAAAGCATCTC	3960
QY	3961	AGGAACATCACTTAGTAGAGAAACAAATGTTCTGTAAGTCTGTTTCTTCAACAGTCA	4020
Db	3961	AGGAACATCACTTAGTAGAGAAACAAATGTTCTGTAAGTCTGTTTCTTCAACAGTCA	4020
QY	4021	GTCGAATGGAAGACTTGACGTCAAAATACAAACCCAGAGATCCTTCTGATTTGGTCTT	4080
Db	4021	GTCGAATGGAAGACTTGACGTCAAAATACAAACCCAGAGATCCTTCTGATTTGGTCTT	4080
QY	4081	CCAAACAAATAGAGCATCACTGTGAAGAGCCAGGAGTGGTCTGAGTAGACAAAGAAATGG	4140
Db	4081	CCAAACAAATAGAGCATCACTGTGAAGAGCCAGGAGTGGTCTGAGTAGACAAAGAAATGG	4140
QY	4141	TTTTCAGATGATGAAGAAAGGAAACGGGCTTGGAAAGAAATATCTAAGAACGAAGCA	4200
Db	4141	TTTTCAGATGATGAAGAAAGGAAACGGGCTTGGAAAGAAATATCTAAGAACGAAGCA	4200
QY	4201	TGGAATTAACCTTAGGTAAGACGACATCTGGGTGTGAAGTGAACAAAGCCTCTCTAG	4260
Db	4201	TGGAATTAACCTTAGGTAAGACGACATCTGGGTGTGAAGTGAACAAAGCCTCTCTAG	4260
QY	4261	ACTGCTTAGGGCTATCTCTCAGAGTGAATTTTAACCACTCAGACAGAGGATACATGC	4320

|||||  
Db 4261 ACAGCTCAGGGCTATCTCTCAGAGTACATTTTAAACCACCTCAGAGGGGATCCCATG 4330  
QY 4321 AACATACCTGATTAAGCTCCAGCAGAAATGCTGAATCTGAAGCTGTGTAGAACGC 4380  
|||||  
Db 4321 AACATACCTGATTAAGCTCCAGCAGAAATGCTGAATCTGAAGCTGTGTAGAACGC 4380  
QY 4381 ATGGAGACCGCTTCTACAGCTACCTTCCATCATAGTACTCTTGGCCCTTGAGG 4440  
|||||  
Db 4381 ATGGAGACCGCTTCTACAGCTACCTTCCATCATAGTACTCTTGGCCCTTGAGG 4440  
QY 4441 ACCTGGAAATCCAGAACAGCATCAGAAAAGAGTATTACTTCCACAGAAAAGTA 4500  
|||||  
Db 4441 ACCTGGAAATCCAGAACAGCATCAGAAAAGAGTATTACTTCCACAGAAAAGTA 4500  
QY 4501 GTGAATACCTATTAAGCCAGAAATCCAGAAAGCCCTTCTGTGACAAAGTTTGAGTGTG 4560  
|||||  
Db 4501 GTGAATACCTATTAAGCCAGAAATCCAGAAAGCCCTTCTGTGACAAAGTTTGAGTGTG 4560  
QY 4561 CAGATAGTTTACCACTGATTAAGAAATTAAGAACAGAGTGAAGAGTCAATCCCTTCTAAT 4620  
|||||  
Db 4561 CAGATAGTTTACCACTGATTAAGAAATTAAGAACAGAGTGAAGAGTCAATCCCTTCTAAT 4620  
QY 4621 GCCCATCATTAAGATAGTGTGAGTACAGAGTGTGCTGCGGAGCTTCAGAAATGAA 4680  
|||||  
Db 4621 GCCCATCATTAAGATAGTGTGAGTACAGAGTGTGCTGCGGAGCTTCAGAAATGAA 4680  
QY 4681 ACTACCATCTCAAGAGAGCCTATTAAAGTGTGTGATGTGAGAGCAACAGCTGGAAG 4740  
|||||  
Db 4681 ACTACCATCTCAAGAGAGCCTATTAAAGTGTGTGATGTGAGAGCAACAGCTGGAAG 4740  
QY 4741 AGCTGTGGCCACACGATTTACGGAACATCTTACTTCCAGGCAAGATCTAGAGGAA 4800  
|||||  
Db 4741 AGCTGTGGCCACACGATTTACGGAACATCTTACTTCCAGGCAAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACCTGATCTGGAATCAGCCTCTTCTGATGACCCGATCTGATCTCTG 4860  
|||||  
Db 4801 CCCCTTACCTGATCTGGAATCAGCCTCTTCTGATGACCCGATCTGATCTCTG 4860  
QY 4861 AAGACAGAGCCCCAGAGTCACTGCTGTGTGGCAACATACCATCTTCAACCTCTGATGA 4920  
|||||  
Db 4861 AAGACAGAGCCCCAGAGTCACTGCTGTGTGGCAACATACCATCTTCAACCTCTGATGA 4920  
QY 4921 AAGTCCCAATTAAGAGTGTGCAAGATCTGCCAGAGTCCAGCTGCTCATACTG 4980  
|||||  
Db 4921 AAGTCCCAATTAAGAGTGTGCAAGATCTGCCAGAGTCCAGCTGCTCATACTG 4980  
QY 4981 ATACTGCTGGGTATATGCAATGGAAGAGTGTGAGAGGAGAGGCAAGATTTGACAG 5040  
|||||  
Db 4981 ATACTGCTGGGTATATGCAATGGAAGAGTGTGAGAGGAGAGGCAAGATTTGACAG 5040  
QY 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGTGTGTGCTGAGCTGACCCAGAG 5100  
|||||  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGTGTGTGCTGAGCTGACCCAGAG 5100  
QY 5101 AATTATGCTGCTGTGCAAGTGTGCAAGAAACACCATCTTAACTAATCTAATTA 5160  
|||||  
Db 5101 AATTATGCTGCTGTGCAAGTGTGCAAGAAACACCATCTTAACTAATCTAATTA 5160  
QY 5161 CTGAAGAGACTCTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTAAGCGGACAG 5220  
|||||  
Db 5161 CTGAAGAGACTCTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTAAGCGGACAG 5220  
QY 5221 TGAATAATTTTCTAGGAATTCGCGAGGAAATGGGTAGTACTAATTTCTGGGTGACCC 5280  
|||||  
Db 5221 TGAATAATTTTCTAGGAATTCGCGAGGAAATGGGTAGTACTAATTTCTGGGTGACCC 5280  
QY 5281 AGCTATTTAAAGAAATAATCTGATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
|||||  
Db 5281 AGCTATTTAAAGAAATAATCTGATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
QY 5341 TCAATGGAAGAAACCAAGGTCCAAAGGAGCAAGAGAAATCCAGAGAGAAAGATCT 5400  
|||||

Db 5341 TCAATGGAAGAAACCAAGGTCCAAAGGAGCAAGAGAAATCCAGAGAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTGCTATAGGGCCCTTCAACAACATGCCCCAGATCAACTGG 5460  
|||||  
Db 5401 TCAGGGGGCTAGAAATCTGTGCTATAGGGCCCTTCAACAACATGCCCCAGATCAACTGG 5460  
QY 5461 AATGATGTACAGCTGTGTGTGCTTGTGTGTAAGAGCTTTCATATCCCTTG 5520  
|||||  
Db 5461 AATGATGTACAGCTGTGTGTGCTTGTGTGTAAGAGCTTTCATATCCCTTG 5520  
QY 5521 GCACAGGTCCACCAATGTGTGTGTGAGCCAGATGCTGAGAGAGCAAGTGGCT 5580  
|||||  
Db 5521 GCACAGGTGTCCACCAATGTGTGTGTGAGCCAGATGCTGAGAGAGCAAGTGGCT 5580  
QY 5581 TCCATGCAATTTGGCAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGTGTGACA 5640  
|||||  
Db 5581 TCCATGCAATTTGGCAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGTGTGACA 5640  
QY 5641 GTGTAGCACTCTACAGAGTGTGAGGCACTGTGTGTGACCCGAGAGTGGTGTGACA 5700  
|||||  
Db 5641 GTGTAGCACTCTACAGAGTGTGAGGCACTGTGTGTGACCCGAGAGTGGTGTGACA 5700  
QY 5701 GCCACTACTGA 5711  
|||||  
Db 5701 GCCACTACTGA 5711

Search completed: May 27, 1999, 20:13:25  
Job time: 11965 sec

GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 1999, 13:24:55 ; Search time 2617.04 Seconds

(without alignments)  
3328.837 Million cell updates/sec

Title: US-08-798-691A-3

Perfect score: 5711  
Sequence: 1 AGCTCGCTGAGACTTCTCTG.....TCCCCACAGCCACTACTGA 5711

Scoring table:

Search: 2002476 segs, 762712212 residues

Database :

EST: \*  
1: em\_est1:\*  
2: em\_est2:\*  
3: em\_est3:\*  
4: em\_est4:\*  
5: em\_est5:\*  
6: em\_est6:\*  
7: em\_est7:\*  
8: em\_est8:\*  
9: em\_est9:\*  
10: gb\_est1:\*  
11: gb\_est2:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: gb\_est6:\*  
16: gb\_est7:\*  
17: gb\_est8:\*  
18: gb\_est9:\*  
19: gb\_est10:\*  
20: gb\_est11:\*  
21: gb\_est12:\*  
22: gb\_est13:\*  
23: gb\_est14:\*  
24: gb\_est15:\*  
25: gb\_est16:\*  
26: gb\_est17:\*  
27: gb\_est18:\*  
28: gb\_est19:\*  
29: gb\_est20:\*  
30: gb\_est21:\*  
31: gb\_est22:\*  
32: em\_est1:\*  
33: em\_est2:\*  
34: em\_est3:\*  
35: em\_est4:\*  
36: em\_est5:\*  
37: em\_est6:\*  
38: em\_est7:\*  
39: em\_est8:\*  
40: em\_est9:\*  
41: em\_est10:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
C	1	492.8	8.6	518	26	AA804632	OB98404.s
C	2	491.8	8.6	523	25	AA702344	AA702344 z187e03.s

RESULT	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45								
AA804632/c	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2								
LOCUS	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2						
DEFINITION	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2					
ACCESSION	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2					
NID	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2					
KEYWORDS	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2					
SOURCE	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2					
ORGANISM	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2					
REFERENCE	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2				
AUTHORS	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2		
TITLE	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2		
JOURNAL	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	
COMMENT	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2	472.2

#### ALIGNMENTS

RESULT 1  
AA804632 518 bp mRNA  
LOCUS OB98404.s1 NCI-CGAP GCBI Homo sapiens CDNA clone IMAGE:139399  
DEFINITION similar to gb:U14680 BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN  
(HUMAN); mRNA sequence.

ACCESSION AA804632  
NID g2876033  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 518)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

CDNA library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/ULNL at:  
[www-bio.lnl.gov/bdnp/image/image.html](http://www-bio.lnl.gov/bdnp/image/image.html)

Insert Length: 2057    Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 460.

```

1..518
/organism="Homo sapiens"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Merli (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-TGTTCACATCTCAAGATGGAGCGGCCCTCATTTTTTTTTTTT-
3'). Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Ronaldo."
/db_xref="taxon:9606"
/clone="IMAGE:1339399"
/clone_1kb="NCI CGAP-GCB1"
/tissue_type="germinal center B cell"
/lab_host=DH10B
97 c 91 g 210 t

```

BASE COUNT	120 a	97 c	91 g	210 t
CRICIN				

**ORIGIN**

Query Match	8.6%	Score 492.8;	DB 26;	Length 518;
Best Local Similarity	99.2%;	Pred. No. 2.8e-113;		
Matches 516; Conservative	0;	Mismatches 2;	Indels 2;	Gaps 2

Oy	1556	AAATCTAAATTAAGGACATTTTCTACTGAGCCAGATTAATCAAGAGGCTCCCTCAC	1615
Db	518	AAATCTAAATTAAGGACATTTTCTACTGAGCCAGATTAATCAAGAGGCTCCCTCAC	460
Oy	1616	AAATAAATTTAAAGCGTAAAAAGAGACCTACATCAGGCTTCATCCTGAGGATTTTATCAA	1675
Db	459	AAATAAATTTAAAGCGT - AAAGAGACCTACATCAGGCTTCATCCTGAGGATTTTATCAA	401
Oy	1676	GAAACGAGTTTGGCAGTTCAAAAGAGCTCCTGAATGATPAATCAGGGAATTAACCAAC	1735
Db	400	GAAACGAGTTTGGCAGTTCAAAAGAGCTCCTGAATGATPAATCAGGGAATTAACCAAC	341
Oy	1736	GGAGCAGATGCTCAAGTATGATGAATTTACTATATGTTGTCATGAGATGAATAAACAAAAG	1795
Db	340	GGAGCAGATGCTCAAGTATGATGAATTTACTATATGTTGTCATGAGATGAATAAACAAAAG	281
Oy	1796	TGATTCATATTCGAATGAGAAAAATCCTTAACCCATAGATGATCACTCGAAAAAGATCTGC	1855
Db	280	TGATTCATATTCGAATGAGAAAAATCCTTAACCCATAGATGATCACTCGAAAAAGATCTGC	221
Oy	1856	TTTCAAAGCGAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAAGTGGAAATTAA	1915
Db	220	TTTCAAAGCGAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAAGTGGAAATTAA	161
Oy	1916	TATCCACATTTCAAAGCAGCTAAAAAGAAATAGGGTGAGAGAGAGTCTTACACAGGA	1975
Db	160	TATCCACATTTCAAAGCAGCTAAAAAGAAATAGGGTGAGAGAGAGTCTTACACAGGA	101
Oy	1976	TATTCATCGCGCTGTAAGTAGTAGTCAGTGAAGATCTAAGCCCACTTAATTTACTGAATT	2035
Db	100	TATTCATCGCGCTGTAAGTAGTAGTCAGTGAAGATCTAAGCCCACTTAATTTACTGAATT	41
Oy	2036	GCAATTTAATGTTGTTCTAGCAGTGAAGAGATTAAGAAA	2075

Db 40 GCAATTGATAGTTGTTCTAGCAGTGAACAGAAAAAAA 1

RESULT	2
AA702344/c	
LOCUS	523 bp mRNA EST 19-DEC-1997
DEFINITION	z187e03.s1 Soares fetal liver spleen INTLS S1 Homo sapiens CDNA c187e03.4 similar to gb:U14680 BRAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN (HUMAN);, mRNA sequence.

**FEATURES**  
**SOURCE**

```

source
1. .523
/organism="Homo sapiens"
/note="Organ: Liver and Spleen; Vector: p7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI
This is a subtracted version of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AACCTGAGAGATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac
I and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
/db_xref="GDB:1352029"
/db_xref="taxon:9606"
/clone="447772"
/clone_1lb="Soares fetal liver spleen INFLS S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"

```

BASE COUNT	127 a	97 c	99 g	200 t
ORIGIN				

## ORIGIN

Query Match	8.68;	Score 491.8;	DB 25;	Length 523;
Best Local Similarity	97.58;	Pred. No. 4.9e-113;		

QY	1527	AGCCTCCCCAATTAGGACATGTAAGTAAATCTTAATATAGAGGACATTTTCTACTAG	1588
Db	523	AGCCTGTGCATCTTAAGCCATGTAGTGCACATTAATTTTAGGAGCATTTGTACTAG	464
QY	1587	CCACAGATAATATACAGAGCGTCCCCCTCACAAATTAATTAAACGCTAAAGAGGACCTACA	1648
Db	463	CCACAGATAATATACAGAGCGTCCCCCTTCAATAATTAATTCAGCGTAAAGAGGACCTACA	404
QY	1647	TCAGGCTTCATCTCTAGAGATTTTATCAAGAAAGCAGATTTGCGAGTTCAAAAAGACTCCT	1708





Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (image.lnl.gov) for further information.  
Seq primer: -28ml3 rev1 ET from Amersham  
High quality sequence stop: 431.  
Location/Qualifiers

## FEATURES

Source

1..444  
/organism="Homo sapiens"  
/note="Vector: Bluescript SK-; Site\_1: EcoRI; Site\_2:  
XhoI; Cloned unidirectionally. Primer: Oligo dt. HeLa S3  
epithelioid carcinoma cells grown to semi-confluency  
without induction. Average insert size: 1.5 kb: Uni-ZAP XR  
vector. -5' adaptor sequence: 5' GAATTCGGCAGCG 3' -3'  
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "  
/db\_xref="taxon:9606"  
/clone="843077"  
/clone\_lib="Stratagene HeLa cell s3 937216"  
/sex="female"  
/dev\_stage="HeLa S3 cell line"  
/lab\_host="SOLR (kanamycin resistant)"  
<1..>444

BASE COUNT 170 a 76 c 86 g 112 t  
ORIGIN

Query Match 7.8%; Score 444; DB 21; Length 444;  
Best Local Similarity 100.0%; Pred. No. 4.6e-101;

Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2997 GCCAAGCAAGTGCATCTTACTCCAAATTAACATGAGCTTTTACCAACCATATCGT 3056  
|||  
Db 1 GGCAAGCAAGTGCATCTTACTCCAAATTAACATGAGCTTTTACCAACCATATCGT 60  
|||  
OY 3057 ATACCAACCTTTTCCATCAAGTCAATTTGTTAAAGTAAGTAAGTAAGTAAGTAAG 3116  
|||  
Db 61 ATACCAACCTTTTCCATCAAGTCAATTTGTTAAAGTAAGTAAGTAAGTAAGTAAG 120  
|||  
OY 3117 GAGGAAACTTGGAGAAATTCATGTCACCGAAGAAAGAAATGGAAATGGAACATT 3176  
|||  
Db 121 GAGGAAACTTGGAGAAATTCATGTCACCGAAGAAAGAAATGGAAATGGAACATT 180  
|||  
OY 3177 CCACGTACAGTGCAGCAATTAAGCCGTAAATTAACATTAAGAAAGCC 3236  
|||  
Db 181 CCACGTACAGTGCAGCAATTAAGCCGTAAATTAACATTAAGAAAGCC 240  
|||  
OY 3237 AGCTCAACATTAATTAAGTACAGTTCAGTACTAATGAAGTGGCTCCAGTATTAA 3296  
|||  
Db 241 AGCTCAACATTAATTAAGTACAGTTCAGTACTAATGAAGTGGCTCCAGTATTAA 300  
|||  
OY 3297 GAAATAGGTTCCAGTGAAGAAACATTTCAAGCAGAACTAGTGAAGAAAGAGGCCAAAA 3356  
|||  
Db 301 GAAATAGGTTCCAGTGAAGAAACATTTCAAGCAGAACTAGTGAAGAAAGAGGCCAAAA 360  
|||  
OY 3357 TTGAATGCTATGCTTAGATTAGGGTTTGAACCTGAGGTCTATTAACAAAGTCTTCT 3416  
|||  
Db 361 TTGAATGCTATGCTTAGATTAGGGTTTGAACCTGAGGTCTATTAACAAAGTCTTCT 420  
|||  
OY 3417 GGAAGTAATTGTAGCAATCTGAA 3440  
|||  
Db 421 GGAAGTAATTGTAGCAATCTGAA 444

RESULT 5  
AA814998 488 bp mRNA EST 05-MAR-1998  
LOCUS  
DEFINITION  
0007905.s1 NCI-CGAP GCBI Homo sapiens cDNA clone IMAGE:1340216 3'  
similar to gb:014680 BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN  
(HUMAN);, mRNA sequence.

## ACCESSION

AA814998  
NID  
KEYWORDS  
SOURCE

## ORGANISM

Homo sapiens  
human.

## REFERENCE

Enkaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 488)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

## AUTHORS

Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.lnl.gov/db/rp/image/image.html](http://www.bio.lnl.gov/db/rp/image/image.html)

## JOURNAL

COMMENT

## FEATURES

Source

Insert Length: 916 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 329.  
Location/Qualifiers

1..488

/organism="Homo sapiens"  
/note="Vector: pRT73D-Pac (Pharmacia) with a modified  
polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, 19D-),  
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was  
primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAGAGGAGGCGCCCTCATTTTCTTTTCTTTT-  
3']. Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
/db\_xref="taxon:9606"  
/clone="IMAGE:1340216"  
/clone\_lib="NCI-CGAP GCBI"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
BASE COUNT 108 a 87 c 94 g 199 t  
ORIGIN

Query Match 7.7%; Score 437.4; DB 27; Length 488;  
Best Local Similarity 97.1%; Pred. No. 2.2e-99;  
Matches 477; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

OY 1587 CCACGATTAATCAAGACGCTCCCTCAAAATTAAGCTTAAGAGAGACTTACA 1646  
|||  
Db 488 CCACGATTAATCAAGACGCTCCCTCAAAATTAAGCTTAAGAGAGACTTACA 429  
|||  
OY 1647 TCAGGCTTCATCCGAGGATTTTATCAAGAAACAGATTTGCGAGTCAAAAGACTCCT 1706  
|||  
Db 428 TCAGGCTTCATCCGAGGATTTTATCAAGAAACAGATTTT-GCAGTCAAAAGACTCCT 370  
|||  
OY 1707 GAAATGATTAATCAAGCAATCAACCAAGCAGAGATGTCAGTGAATGATTAATCT 1766  
|||  
Db 369 GAAATGATTAATCA- GGAATCAACCAACCAAGCAGAGATGTCAGTGAATGATTAATCT 311  
|||  
OY 1767 AATAGTGTCTATGCAATTAACAAAGGCTGATTTCTATTGAGATGAGAAAAATCTTAAC 1826  
|||  
Db 310 AATAGTGTCTATGCAATTAACAAAGGCTGATTTCTATTGAGATGAGAAAAATCTTAAC 251  
|||

QY 1827 CCATAGAACTACTCGAAAAAGAAATCTGCTTTTCAAAAAGAAAGCTGACCTATATAGCAGC 1886  
 Db 250 CCAATAGAAATCAGTCGAAAAAGAAATCTGCTTTTCAAAAAGAAAGCTGACCTATATAGCAGC 191  
 QY 1887 AGATATAGCAATATGAACTGAAATTAATATCCAAATTCAAAAGCACTTAAAGAAAT 1946  
 Db 190 AGATATAGCAATATGAACTGAAATTAATATCCAAATTCAAAAGCACTTAAAGAAAT 131  
 QY 1947 AGCTGAGAGAGAAAGCTTCTACACGAGCATATTCATCGCTTGAACTAGTACGTAGAGA 2006  
 Db 130 AGCTGAGAGAGAAAGCTTCTACCA-CCATATTCATTCGCTTGAACTAGTACGTAGAGA 72  
 QY 2007 AATCTAAGCCACCTAATTTACTGAAATTCGAAATGATAGTTCTTCTAGCAGTGAAGAG 2066  
 Db 71 AATCTAAGCCACCTAATTTACTGAAATTCGAAATGATAGTTCTTCTAGCAGTGAAGAG 12  
 QY 2067 ATAAAGAAAA 2077  
 Db 11 ATAAAGAAAA 1

RESULT 6  
 AA484941 429 bp mRNA EST 15-AUG-1997  
 LOCUS aa41808.r1 NCI-CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:815798 5'  
 DEFINITION similar to gb:014680 BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN  
 (HUMAN);, mRNA sequence.  
 ACCESSION AA484941  
 NID 92214160  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;  
 Homo.  
 1 (bases 1 to 429)  
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
 Ph.D., Gerald Marti, M.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www.bio.lnl.gov/bdip/image/image.html  
 Seq primer: -28m13 rev1 ET from AmerSham  
 High quality sequence stop: 414.  
 Location/Qualifiers  
 1. 429  
 /organism="Homo sapiens"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was prepared from human tonsillar cells enriched for  
 germinal center B cells by flow sorting (CD20+, IgD-),  
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
 primed with a Not I - oligo(dT) primer  
 [5'-TGTTCACCAATCTGAAGTGGAGCGCGCTCATTTTCTTTTCTTTT-  
 3']. Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

/db\_xref="taxon:9606"  
 /clone="IMAGE:815798"  
 /clone\_1ib="NCI-CGAP\_GCB1"  
 /tissue\_type="germinal center B cell"  
 /lab\_host="DH10B"  
 <1..>429  
 /db\_xref="GDB:6035419"  
 BASE COUNT 153 a 70 c 101 g 105 t  
 ORIGIN

Query Match 7.4%; Score 421.8; DB 21; Length 429;  
 Best Local Similarity 99.5%; Pred. No. 1,7e-95;  
 Matches 423; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2311 AACAGAGAACTAGAAACAGTTAAAGTGTCTATATATGCTGAAGACCCCAAGATCTCA 2370  
 Db 5 AGGAGAGAAACTAGAAACAGTTAAAGTGTCTATATATGCTGAAGACCCCAAGATCTCA 64  
 QY 2371 TGTTAAGTGGAGAAAGGTTTGCAGAACTGAAAGATCTGAGAGAGTAGCAGTATTTCT 2430  
 Db 65 TGTTAAGTGGAGAAAGGTTTGCAGAACTGAAAGATCTGAGAGAGTAGCAGTATTTCT 124  
 QY 2431 TGGTACTGCTAGTGAATTAAGCAGCAGTAAAGTATCTGCTAGTACGAGTAGCAGTCT 2490  
 Db 125 TGGTACTGCTAGTGAATTAAGCAGCAGTAAAGTATCTGCTAGTACGAGTAGCAGTCT 184  
 QY 2491 TAGGAAAGCCAAACAGAAACCAATTAATGTGTGATCAGTGTGAGCATTTTGAAGACC 2550  
 Db 185 TAGGAAAGCCAAACAGAAACCAATTAATGTGTGATCAGTGTGAGCATTTTGAAGACC 244  
 QY 2551 CCAAGGACTAATTCATGTGTGTTCCAAAGATATATGAAATGACACAGAGCCTTTAAGT 2610  
 Db 245 CCAAGGACTAATTCATGTGTGTTCCAAAGATATATGAAATGACACAGAGCCTTTAAGT 304  
 QY 2611 ATCCATTGGGACATGAAAGTAAACCAACAGTGGGAAACACCATATAGAAATGAAAGAGT 2670  
 Db 305 ATCCATTGGGACATGAAAGTAAACCAACAGTGGGAAACACCATATAGAAATGAAAGAGT 364  
 QY 2671 AACTGTATGCTCAGTATTTTGCAGAAATATCATTCAGAGTTTCAAGCGCCAGTCTTGGCT 2730  
 Db 365 AACTGTATGCTCAGTATTTTGCAGAAATATCATTCAGAGTTTCAAGCGCCAGTCTTGGCT 424  
 QY 2731 TGTTT 2735  
 Db 425 CGTTT 429

RESULT 7  
 A1040685/c 459 bp mRNA EST 28-AUG-1998  
 LOCUS A1040685  
 DEFINITION oxi18B06.s1 Soares fetal liver spleen INF5.s1 Homo sapiens cDNA  
 clone IMAGE:155659.3 similar to gb:014680 BREAST CANCER TYPE 1  
 SUSCEPTIBILITY PROTEIN (HUMAN);, mRNA sequence.  
 ACCESSION A1040685  
 NID 93279879  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 459)  
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Trace considered overall poor quality



Db 301 AACGAGATGTTGACTGGAAGAAATCACCAGGTCACGAGATCCAGAAATCCCGG 360  
 QY 5389 ACAGAAAGATCTTCAGGGGCTAGAAATCTGTTGCTATGGGCTTCACCAAGATGCCCA 5448  
 Db 361 A---AAAGCTCTCAAGGGCTACAGGCTATATGTTGTAGCCCTTACCAACATGCCCA 417  
 QY 5449 CAGATCACTGGAATGATGATACAGCTGTGTGCTCTGTGTGTGAGAGAGCTTTCAT 5508  
 Db 418 AAGATAGCTGAGAGAGATCTGAGCTGTGTGGGCTTCCTGAGAGAGCTTTCAT 477  
 QY 5509 CATTACCCCTTGGACAGAGTGTCCACCAATTTGTTGTGTGAGCCAGATGCCGTGACAG 5568  
 Db 478 CGCTACCCCTGACACAGGCTGCTATCTATGATGATGACAGCAG-CGCTGGACAG 536  
 QY 5569 AGGACATGCTTCATCATGATGATGAGGAGATGTTGTGAGCAGCTGTGTGACCCAGACT 5628  
 Db 537 AAGACACACATGCGCCAGATATGAGGAGCTGTGTGAGCAGCAGCAGCTGTGTGATGTGACT 596  
 QY 5629 GGGTGTGGACAGTGTGACACTCTACCACTG 5659  
 Db 597 GGGTGTGGACAGTGTATCCAGTACCCGTG 627

RESULT 9  
 A1016870 466 bp mRNA EST 16-JUN-1998  
 LOCUS ou31a01.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens CDNA clone  
 DEFINITION IMAGE:1627848 3' similar to gb:U14680 BREAST CANCER TYPE 1  
 SUSCEPTIBILITY PROTEIN (HUMAN);, mRNA sequence.

ACCESSION A1016870  
 NID 93231206  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 466)  
 REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT

FEATURES  
 source  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 This clone is available royalty-free through LNLN; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seg primer: -40m3 fwd. ET from Amersham  
 High quality sequence stop: 140.  
 Location/Qualifiers

1. 466  
 /organism="Homo sapiens"  
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
 a modified polylinker; Site.1: Not I; Site.2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung, NDHL19w, testis NHT, and B-cell  
 NCI-CCAP\_GCB1) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I.M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Boudado."  
 /db\_xref="taxon:9606"  
 /db\_xref="IMAGE:1627848"  
 /clone\_1lb="Soares\_NFL\_T\_GBC\_S1"  
 /lab\_host="DH10b"

BASE COUNT 116 a 90 c 99 g 161 t  
 ORIGIN

Query Match 5.8%; Score 330.4; DB 28; Length 466;

Best Local Similarity 90.8%; Pred. No. 1,5e-72;  
 Matches 363; Conservative 0; Mismatches 36; Indels 1; Gaps 1;

QY 1668 TTTATCAGAAAGACAGATTGGCAGTTCAAAAGACCTCGAATGATTAATCAGGAACT 1727  
 Db 400 TTTTCTAGAAAGACACATTGGCAGTTTAAAGACCTCTGTAATGATATATCAGGGACT 341  
 QY 1728 AACCAACGGAGAGAGATGGTCAAGTATGATTAATTAATAGTGTCTAGAAATAA 1787  
 Db 340 AACCAACGGAGCGAATGGTCCAGTATGATTAATTAATAGTGTCTAGAAATAA 281  
 QY 1788 ACAAAAGTATCTTATTCAGATGAGAAAATCCCAACCATAGATACCGAATAA 1847  
 Db 280 ACAAAAGTATCTTATTCAGATGAGAAAATCCCAACCATAGATACCGAATAA 221  
 QY 1848 GAATTCCTTTCAAAAGCAAGCTGAACCTA-TAAGCAGCATATAACATATGAACT 1906  
 Db 220 GAATTCCTTTCAAAAGCAAGCTGAACCTA-TAAGCAGCATATAACATATGAACT 161  
 QY 1907 CGAATTAATATCCACATCAAAAGCAGCTTAAGATAGCTGAGAGAACTTTC 1966  
 Db 160 GGAATTAATATCCCAATTCAAAAGCAGCTTAAGATAGCTGAGAGAACTTTC 101  
 QY 1967 TACCAGCATATTCATGCGCTTGAATGATGATGATGATGATGATGATGATGATG 2026  
 Db 100 TACCAGCATATTCATGCGCTTGAATGATGATGATGATGATGATGATGATGATG 41  
 QY 2027 TACTGAATTCGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2066  
 Db 40 TACTGAATTCGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1

RESULT 10  
 AA205474 418 bp mRNA EST 27-JAN-1997  
 LOCUS z66b05.f1 Striatogene neuroepithelium (#37231) Homo sapiens CDNA  
 DEFINITION clone 646545 5' similar to gb:U14680 BREAST CANCER TYPE 1  
 SUSCEPTIBILITY PROTEIN (HUMAN);, mRNA sequence.

ACCESSION AA205474  
 NID 91803464  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Eukaryota; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 418)  
 REFERENCE Hillier,L., Clark,N., Dubuque,T., Eliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevisan,E.,  
 Waterston,R., Williamson,A., Wohlmann,P. and Willson,R.  
 WashU-Merk EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT

FEATURES  
 source  
 Contact: Willson RK  
 WashU-Merk EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 This clone is available royalty-free through LNLN; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seg primer: -28m3 rev2 from Amersham  
 High quality sequence stop: 284.  
 Location/Qualifiers

1. 418  
 /organism="Homo sapiens"  
 /note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:  
 XhoI; Cloned unidirectionally. Primer: Oligo dt. NT2  
 cells (Mera-2/cl.D1) induced with Retinoic Acid for 24  
 hours. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5'  
 adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor  
 sequence: 5' CTCGAGTCTTTTCTTTTCTTTTCTTTT 3'."







OY	1970	CAGGATATTTCACGGCCTTGACTAGTACGTAGCAAAATCTAAGCCACCATAATTGTAC	2029
Db	1	CAGGCATATTTCATNCGCTTGAACTAGTAGTACATAGAAAATCTAAGCCACCCTTAATGTCC	60
OY	2030	TGAATTTGCCAAATGTAGTGTGTTCTCATGACAGTGAAGAGATTAAGAAAAAAGTACAACCA	2089
Db	61	TGAATTTGCCAAATGTAGTGTGTTCTARCAAGTGAAGAAGATTAAGAAAAAAGTACAACCA	120
OY	2090	AATGCCAGTCAGGCGACAGCAAGAAACCTACACATCTCATGGAAGGTAAAGAACCTGCACACTGG	2149
Db	121	AATGCCAGTCAGGCGACAGCAAGAAACCTACACATCTCATGGAAGGTAAAGAACCTGCMACTGG	180
OY	2150	AGCCAAGAAAGAGTAAACACAGCCAAATGACAGAC	2182
Db	181	ARCCAAAGAAAG-TAACNAGCCCAATATACAAGAC	212
RESULT	14		
LOCUS	AA985850	717 bp	EST
DEFINITION	ue67a08.r1 BREAST 2NDMT Mus musculus cDNA clone 1362518 5' similar to gb:U036475 Mus musculus breast and ovarian cancer susceptibility protein (MUSE);, mRNA sequence.		
ACCESSION	AA985850		
NID	G3167239		
KEYWORDS	EST.		
SOURCE	Mus mouse. Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 717)		
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubugue,T., Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.		
TITLE	The Mashu-HHMI Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mousesest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. MG1:895738 Seq primer: -28m3 rev2 ET from Amersham High quality sequence stop: 407. Location/Qualifiers 1..717 /organism="Mus musculus" /strain="C57BL/6J" /note="Vector: pRTT3-Pac (pharmacia) with a modified polylinker Site_1: Not I; Site_2: Eco RI; 1st strand CDNN was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAGATGGAGCGCCGCTTTTTTTTTTTTTTTTTTTT 3'] ; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Patima Bonaldo." /db_xref="taxon:10090" /clone="1362518" /contig="lib=Soares 2ndmt" /sex="male" /tissue_type="Thymus" /dev_stage="4 weeks"		

BASE COUNT	175 a	160 c	186 g	196 t
ORIGIN	/lab_host="DHI0B"			
Query Match	2.4%	Score 138.2;	DB 28;	Length 717;
Best Local Similarity	74.5%;	Pred. No. 2.7e-24;		
Matches 187; Conservative	0;	Mismatches 63;	Indels 1;	Gaps 1;
OY	5446	CCACGATCAACTGGATGTAGTGAACCTGTGTCCTCTGTGGTGAGAGAGCTTT	5505	
Db	2	CCAAAGATTAGTGGAGAGAGATGTGCACCTGTGGGGCTTCCTGGGAGAGAGCTTC	61	
OY	5506	CATCATTCACCCTTGGCAGAGGTGTGCCAACCAATGTGGTTGTGGAGCCAGATGCCTGGA	5565	
Db	62	CATCGCTCACCATGACACAGGTGCTCATCTAGTTGTGTANCGTCGACGCCAAGCCCTGGA	121	
OY	5566	CAGAGACACAATGGCTTCATGCATTTGGGAGAGTGTGAGGCACACCTGTGTGACCCGAG	5625	
Db	122	CAGAAGACAGCAACACGCCAGATATTGGGCACCTGTGCMAAGCA-GTCTTGGAGATGTGG	180	
OY	5626	AATGGTGTGGACAGTGTAGACCTCACTCACTGAGCAGAGAGCTGGACACCACTCATGTATG	5685	
Db	181	ACTGGGTGTGGACAGTGTAGATCCACTCACTGCGGTGTGCGGATCTGGATGCTTAACCTGTGAC	240	
OY	5686	CCCAGATCCCC	5696	
Db	241	ACAAATATCACC	251	
RESULT	15			
LOCUS	W82081	507 bp	mRNA	EST
DEFINITION	me6b06.r1 Soares mouse embryo NM013.5 14.5 Mus musculus cDNA			
ACCESSION	W82081			
NID	91539560			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryotes; mtochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 507) Marras,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterson,R.			
TITLE	The WashU-HMT Mouse EST Project			
JOURNAL	Unpublished (1996)			
COMMENT	On Sep 13, 1996 this sequence version replaced gi:1393032.			
FEATURES	Contact: Marra M/Mouse EST Project WashU-HMT Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through INLNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. MG1:247219 Putative full length read vector to vector length is Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 505. Location/Qualifiers 1..507 /organism="Mus musculus" /strain="C57BL/6J" /note="Vector: pUT73D-Pac (Pharmacia) with a modified polylinker. Site:1: Not I; Site:2: Eco RI; 1st strand cDNA			



